FIG. 1

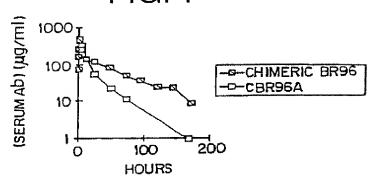
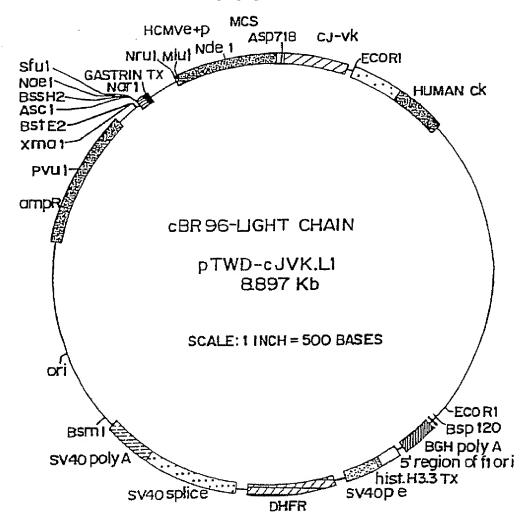


FIG. 2



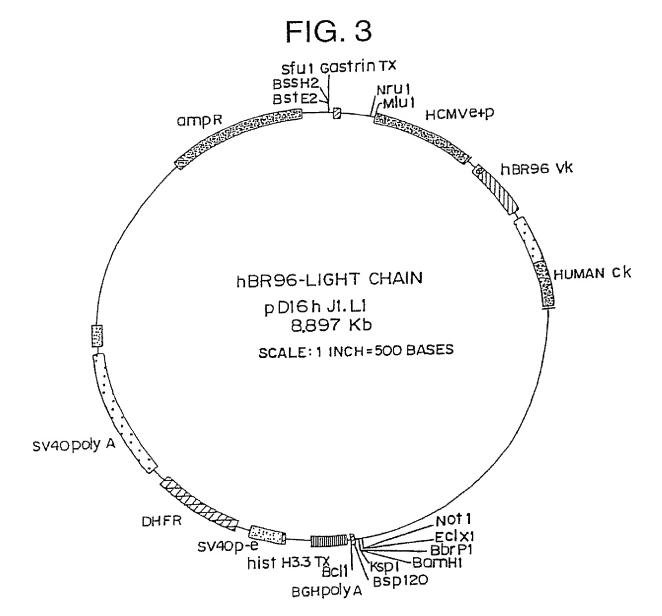


FIG. 4

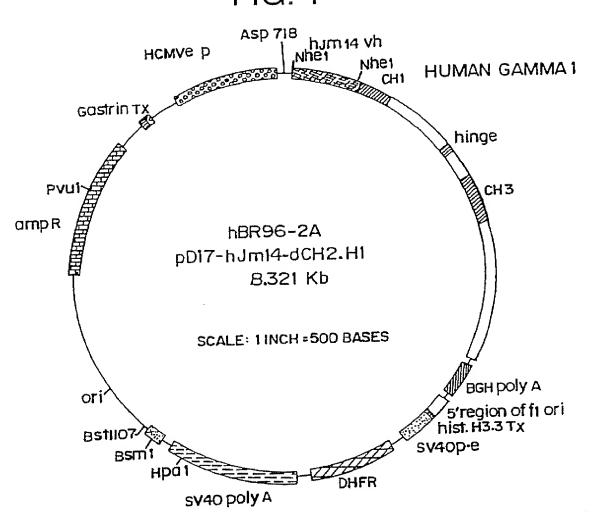


FIG. 5

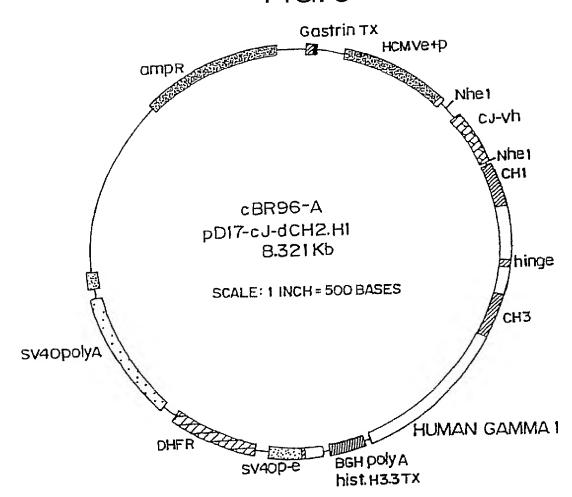


FIG. 6

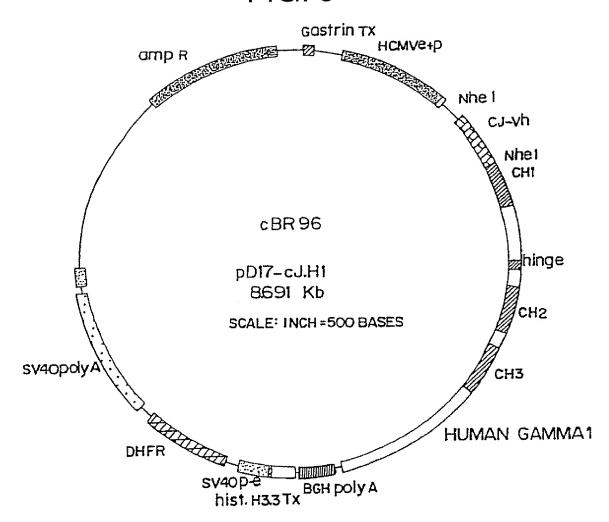


FIG. 7

hBR96-2A DOX

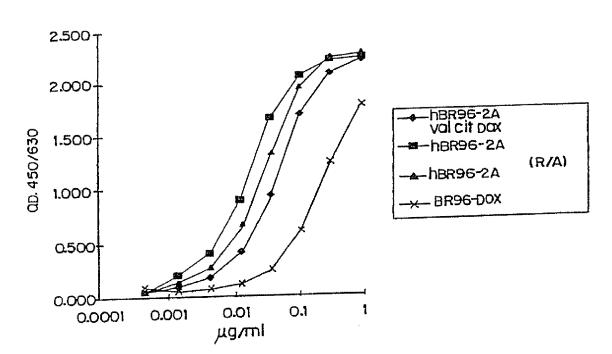
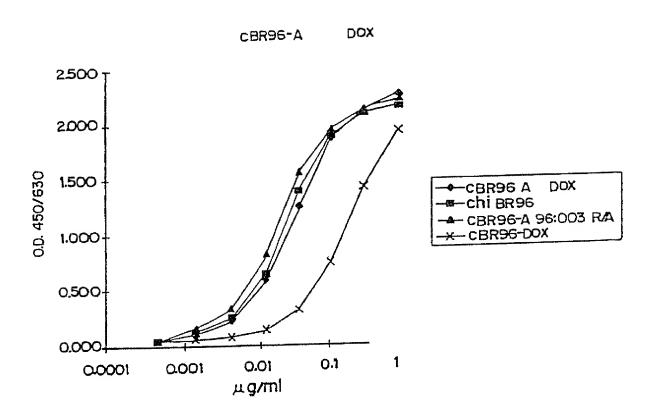
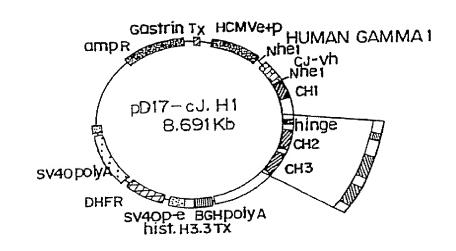


FIG. 8



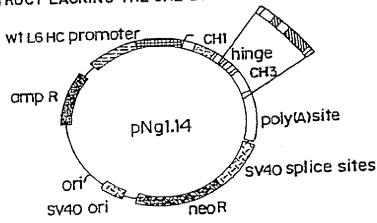
## FIG. 9A

A-HINGE + CH2 + CH3 DOMAINS WERE REMOVED FROM BR96 IGGI CONSTRUCT BY E.CO.47-III RESTRICTION DIGESTION.



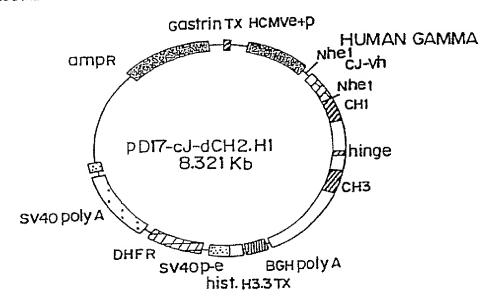
## FIG. 9B

B.-HINGE+CH3 DOMAINS AMPLIFIED BY PCR FROM L6 IGG1 CONSTRUCT LACKING THE CH2 DOMAIN.



## FIG. 9C

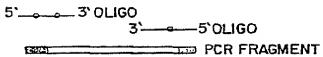
C.-HINGE+CH3 PCR FRAGMENT CLONED BY HOMOLOGOUS RECOMBINATION INTO E.CO.47-III SITE OF BR96 IGGI MOLECULE.



1.- INTRODUCTION OF MUTATIONS BY SITE DIRECTED MUTAGENESIS ON DOUBLE-STRANDED PLASMID DNA.

### **FIG. 10A**

A.- MUTATIONS INTRODUCED INTO SYNTHETIC OLIGONUCLEOTIDES USED FOR THE PCR AMPLIFICATION OF CH2 DOMAIN



## FIG. 10B

B.-PLASMID DNA LINEARIZED INSIDE CH2 DOMAIN AND COTRANSFORMED WITH PCR FRAGMENT INTO COMPETENT DH5a



### FIG. 10C

C. CLONING MEDIATED BY HOMOLOGOUS RECOMBINATION YIELDS TRANSFORMANTS HARBOURING RECOMBINANT PLASMIDS.



FIG. 11

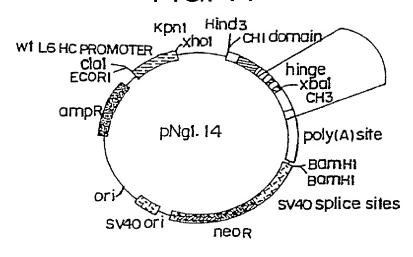


FIG. 12

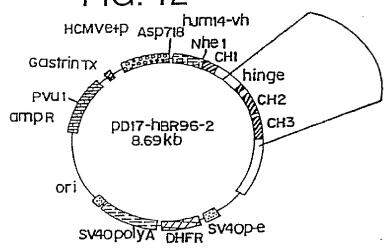


FIG. 13

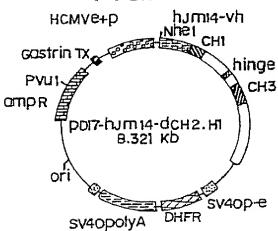


FIG. 14A
Primary Sequence = SEQ ID NO:10
Complementary Sequence = SEQ ID NO:28

Complementary Sequence = SEQ ID NO:28 CGCTGGGAGG GCCACCCTCC AAATGGCCCG TTTACCGGGC ATGGTGATGC TACCACTACG CCCTCAAACA GGGAGTTTGT 540 GGCTGACCGC CCGACTGGCG TGGGTGGACT ACCCACCTGA 450 360 270 AATTGCATGA AGTTATTAAT TCAATAATTA GAACTGGCTG TTAACGTACT AGCCAGTATC TCGGTCATAG TAGGCGTGTA ATCCGCACAT TGACGTCAAT ACTGCAGTTA CAATGACGGT GCGATAATGG CGCTATTACC TIGACGICAA AACTGCAGTT GITTACTGCCA ATTATTGACT CAACTGTAAC TAATAACTGA TGGCCCGCCT ACCGGGCGGA CTTGACCGAC CGCATAGTTA GCGTATCAAT 170 AAATGGGCGG TTTACCCGCC AGGTGGGGTA ATGTAGATGC ATAATCAGTA TCCACCCAT 790 AATGCCATTT CTATTGACGT GATAACTGCA TATTAGTCAT GGACTITCCA CCTGAAAGGT 610 TTACGGTAAA GITCCGITCC 340 GITGACATIG CAAGGCAAGG 160 GCTCTGATGC CGAGACTACG CCATTGACGC GITGAGGCGG GGTAACTGCG TITCCAAGIC AAAGGITTCAG 870 TACATCTACG AGTACGCCCC TCATGCGGGG GTTACATAAC CAATGTATTG ACGCCAATAG TGCGGTTATC AGATATACGC TCTATATGCG TARGCTACAA ATTCGATGTT AGTACAATCT 240 TCATGTTAGA 150 CHACTCCGCC 500 TCCCATAGEA CCCTGAAAGG ATGAACCGTC CTCACGGGGA GAGTGCCCCT TACTIGGCAG 960 TCATATGCCA TAGTICACAT AGTATACGGT 680 AGGGTATCAT ACATGCCCGG GGAGITCCGC CCTCAAGGCG TGTACGGGCC 410 GICGACTCTC GAGCAAAATT CTCGTTTTAB CAGCTGAGAG 230 140 TTACAGCATT AATGTCGTAA AGCGGTTTGA TCGCCAAACT GGGACTTTCC TGACGTATGT ATCAAGTGTA 670 ACTGCATACA GCAAAACGCG ACGAAGCGCT GCCCATATAT CGGGTATATA 490 TGCTTCGCGA TCATCACGCG 310 400 TAGGGGATAC AGTAGTGCGC ATCCCCTATG 220 130 GACTTTCCAA AAACCGTGGT TTTAGTTGCC CTGAAAGGTT 840 GGGCGTGGAT CCCGCACCTA ATGACCTTAT TACTGGAATA TIGGCAGIAC AACCGTCATG 0 9 9 ACCTCAATAA CGTTTTGCGC AATCAAGTAT 480 TGCAGTTATT 570 390 TTAGTTCATA GAGGTCGCTG CTCCAGCGAC CGATCTCCCG GCTAGAGGGC 210 AAATCAACGG CATGTAGTTA TGCCCAGTAC GTACATCAAT ACGGGTCATG AACTGCCCAC TTGACGGGTG 650 CCGCCCATTG TCATTAGTTA ATGCCCCAGT GGCGGGTAAC 560 TAGGGTTAGG TCTTAGACGA ATCCCAATCC TACGGGGGTCA AGTTTGGCGC TTGTGTGTTG AACACACAAC TCAAACCGCG 200 110 TTTGGCACCA CCTGGCATTA GGTTTTGGCA CCAAAACCGT ATTTACGGTA GGACCGTAAT CCAACGACCC GGTTGCTGGG TAAATGCCAT AGTAATCAAT ACGAGGGACG AGAATCTGCT TGCTCCCTGC AAACTCTACC TTTGAGATGG

pD17-cJ-dCH2.H1

AATAAAATAA

TAATTTATT ATTAAAATAA

GGAAAAAAA

CGGTCTCATT

GCTTCGAATA

TCCGCGCGGC

AGGCGCGCCG

AGGTGACCTG

CTCTAGACGA

GAGATCTGCT

GACGGATCGG

GCCAGAGTAA

CCTTTTTTT

CAACCACTCT

CCTGTTCTTT

TGTGGTTCCA

Treggereer

GCACTTAGTG

TGTAGACGTT

Gredanceco recorcidea

ACGGGGAGGTC

TGCCCTCCAG

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#### **FIG. 14B**

### Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

GTTGGTGAGA CACCAGIGGC 1530 TGCCACAGCA GIGGICACCG GTCTTCCCCC GCAAGAGGCC CAGAAGGGGG 1440 CGTTCTCCGG CGATTCACCA 1350 TATTGGCTGA TAGGTCTGTG ACATTTCCCA GCTAAGTGGT 1170 GIACATAACC CAAGCGGICI TCTGGGGGAG CACTICACIT AGACCACCIC AGACCCCCIC GITTCGCCAGA GCTTGCTAGC GAGACCCAAG CGAACGATCG Crcredelire CGAACCGGTG GGACAAGAAA GCTTGGCCAC CCTCAGCAGC GGAGTCGTCG GGGCCCATCG GTATTACTGT CATAATGACA CCCGGGTAGC 1610 1520 1430 TGTAAAGGGT TCTGGTGGAG CATGTATTGG 1340 1160 AGTGATATCC TCTTGCGGCC AGAACGCCGG TCACTATAGG ACACCAAGGT ACTACTICCC TGATGAAGGG GACTCTACTC CTGAGATGAG GTGACTATTA CTAGCACCAA 1600 GATCGTGGTT ACACAGCCAT TGTGTCGGTA 1510 ATCCAGACAC GTGAAGTGAA GCTAACCTTA 1240 AATTATGCTG 1150 CGATTGGAAT TTAATACGAC 1060 CGTGAATCAC AAGCCCAGCA AAGTCTGAGG I CIGGICAAGG CAGTCCTCAG 1770 GTCAGGAGTC GACCAGITCC Grererag CAGAGACATC 1590 1500 ATAACCGACT TTCACTTTCA 1320 GGTGTCCAGT CCACAGGTCA 1230 AAGTGAAAGT 1410 TGGCCAGTTA ACCEGICAAT CTTATCGAAA GAATAGCTTT 1050 CCTGGGCTGC GGCTGTCCTA CCGACAGGAT 1670 GAGCCGTCTG GCCAAGGGAC TCTGGTCACG CGGTTCCCTG AGACCAGTGC GGACCCGACG 1490 AGGTGGTGAT TCCACCACTA CTCGGCAGAC AGGGACTITC AGAGGACACA TIGGAGACCI 1400 AACCTCTGGA 1310 TCTCTAGATA 1220 AGAGATCTAT TGTTTTAAA CGAACCAGGA AGGAACAGGA ACAAATTTT ACGNATGACC TGCTTACTGG 1130 ACATCTGCAA ACACCTTCCC GCACAGCGGC TGTGGAAGGG 1570 CGTGTCGCCG 1660 ACCIGCAAAT TIGIGGGACA IGGACGITIA TGTAATCAGT 1480 ACATTAGTCA TCTCCTGTGT 1390 1210 1300 TCCAGAGCTC TCCTIGICCT AGGTCTCGAG GAGAACCCAC CTCTTGGGTG 1120 AGCGGCGTGC ACCCAGACCT TEGAGACCCC TCGCCGCACG ACCTCTGGGG 1650 CGAATGACCC AACACCCTGT GCTTACTGGG TGGGTCGCAT CTCCGACCTC ACCCAGCGTA TCCCTGAAAG 1290 1380 1470 GCTTGGTCCT ATATCTCCTT TATAGAGGAA TGGCTAACTA ACCGATTGAT 1110 1020 CAGCTTGGGC CGCCCTGACC GCGGGACTGG CTCCAAGAGC GAGGTTCTCG GGCCTGGTTT 1640 GAGGCTGGAG CAATGCCAAG GTTACGGTTC CCGGACCAAA CGGACCTCCC 1460 GCCTGGAGGG 1280 AACACCAATT GTCTCGAGAG ATTTAAATTG TAAATTTAAC TTGTGGTTAA CAGAGCTCTC 1190 1010 GGAACTCAGG CCTTGAGTCC TGGCACCCTC ACCGTGGGAG ACCTGCTGCC CACCATGGAG GTGGTACTC TGGACGACGG CTCCAGAGAA TCTCCAGAGA AGAGGTCTCT GAGGTCTCTT GCTTAGTGCA CGAATCACGT 1180 CTTGGTACCA GAACCATGGT TCTATATAG AGATATATTC

#### FIG. 14C

### Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

ACACGCAGAA TGTGCGTCTT 2430 ACATCGCCGT TCTACAGCAA 2340 AGATGTCGTT CACAGGTGTA GTGTCCACAT TGTAGCGGCA GCCACATGGA CGGTGTACCT 2160 CCAGGCCTCG GGTCCGGAGC CTCGGTATAG GGTCTAAGGT TCAGGTCCCG TITICCCCAG AAAAGGGGTC GAGCCATATC CCAGATTCCA ChCAACCACT GGCACTACGT ACTCCGAGAC GTGTTGGTGA GITICCGAAG ATAGGGICGC TCCTTCCTCC TATCCCAGCG GAGGCTGCCG AGGAAGAAGG CCCCGAGAAC CATTCGGTCG CATGTCCGGA GGGGCTCTTG GTAAGCCAGC GTACAGGCCT TTCTCTCCTC AAGAGAGGAG 2420 GACCTGCCAA AGAAGACCGA CTGGACGGTT ATGCAGCCCC TCTTCTGGCT TACGICGGG CICCGACGGC TGAGGCTCTG CAAAGGCTTC 2680 TACAGGGCAG ATGTCCCGTC CCGTGCCCAG TGGGTACCAA ACCCATGGTT GAGCCTGTGG GGCACGGGTC 2320 2140 CTCGGACACC 2410 GTAGGGCCGA AGGGAGAGGG TCCCTCTCCC GCTGGGCTCA CGACCCGAGT CATCCCGGCT 1960 1870 CCGTGATGCA GGACGGACCA GGAGACAGGG CCGTGCTGGA GGCACGACCT 2670 CCTCTGTCCC 2580 ACACACCACG TGTGTGCTGC CCTGCCTGGT 2400 TGAGGGAGTC CACATGCCCA GTGTACGGGT TGAGTACGAG ACTCCCTCAG ACTCATGCTC AGGGGCAGGT TCCCCGTCCA 2130 2310 2040 TGCCTGGACG AGTCGCGAGG ACGGACCTGC 1950 CCCCTTGCAG AAGAGTACGA TTCTCATGCT TGGTGCGGAG 2480 ACCACGCCTC CGACATGGTT GTCAGCCTGA CAGTCGGACT GCATCCAGGG CGTAGGTCCC 2390 GCTGTACCAA TGITTIGAGI CAAACTCTCC ACAAAACTCA 2300 CTGCACACAA GTTTGAGAGG TGCCCGCCCC ACGGGCGGG 2030 GACGTGTGTT TCAGGGGTCC 1940 GGGGAACGTC CAACTACAAG 2650 GTTGATGTTC GAGAGTGACC CTCTCACTGG CAAGAACCAG GTTCTTGGTC TCTCATCGGA AAATCTTGTG TTTAGAACAC AGAGTAGCCT 2380 2290 2470 AACCCAGGCC CCCCAAAGGC GGGGTTTCCG TTGGGTCCGG 2110 2200 GAAGCCAGGC 1930 CGGAGGCCTC GCCTCCGGAG 2020 CTTCGGTCCG CCACCGTCGT GGTGGCAGCA TACTCGACTG AGCCGGAGAA TCGGCCTCTT ATGAGCTGAC CAGGTGCCCT GGAGACGGGA GTCCACGGGA 2370 CCTCTGCCCT TGCAGAGCCC ACGTCTCGGG 2280 2460 2190 TCCACGGGGA CCTAAGCCCA GGATTCGGGT AGGTGCCCCT 2100 GTGTCTGCTG CCTCTTCACC 2010 CACAGACGAC 1920 GGAGAAGTGG CTGTTCTCGT GACAAGAGCA GGTAGGGCCC AGCAATGGGC TCGTTACCCG 2630 CCATCCCGGG CTCGGCCCAC GAGCCGGGTG CAAGGCGGGA GTTCCGCCCT 2450 2540 TAGAAGAGAG CTGCCCCTGA GACGGGGACT 2180 ATCTTCTCT 2270 GCCCCGTCTG GGCACAGGCT CCGTGTCCGA 2090 CGGGGCAGAC GGGAGGGAGG CCCTCCCTCC 1910 GCTCACCGTG CGAGTGGCAC GGAGTGGGAG CCTCACCCTC CACCCTGCCC GTGGGACGGG CCCTCCAGCT CAGAGGCCGG GTCTCCGGCC GTAACTCCCA CATTGAGGGT GGGAGGTCGA CGGGAGGACC GCCCTCCTGG 2170 AGCAAGGCAG TCGTTCCGTC GCTCTGGGCA CGAGACCCGT GCCAGCACA CCGGTCGTGT

#### **FIG. 14D**

Primary Sequence = SEQ ID NO:10

Complementary Sequence = SEQ ID NO:28 TCAGACAAAC AGTCTGTTTG 3150 3240 3330 CCTGTGGAGG GGACACCTCC CACCACACAC Greerere GRACACTCCT CTTGTGAGGA CTACCCCCAC GATGGGGGGTG 3060 Trerereace AAGACACTCG 2970 TGTGCAGGTG ACACGICCAC AGCAGCACCT TCGTCGTGGA TACCAAGAAA TGCTTGGCAC ATGGTTCTTT ACGAACCGTG GCTGACCTGC CGACTGGACG CTGACAGGAC ACTCTCGGGC GCCACACGGC TCGCACACGT GGAGTGGGTA CCCCTGTACG TGAGAGCCCG GACTGTCCTG CCTCACCCAT 3410 CGGTGTGCCG AGCGTGTGCA CCCTCCCTCC GGGAGGGAGG 3140 3320 ACCEGETTCC 3050 3230 CGAGACTGTG GCTCTGACAC TGGCCCAGGC CGCACGAGGA dcgrdcrccr 2960 TICICCACAT AAGAGGTGTA GGGGACATGC 3400 AGGITGGCCG AGCAAGGICC TCGTTCCAGG ACAGGCCCTC TCCAACCGGC 3220 TGTCCGGGAG 3490 CGGTCGCACC CTCTGTAGGA GAGACATCCT CAGGGGTGTG 3040 GCCAGCGTGG 3310 GTCCCCACAC ACCCGGGGGAC 3130 2860 TGGGCCCCTG CTCTCGCGGT GAGAGCCCA 2950 CCCCGCACTG CCCAGACCAG TCTCGGCAGC AGAGCCGTCG GGGTCTGGTC 3570 AACCGACTCC GGGGCGTGAC 3480 3300 TTGGCTGAGG ACCCCCTAAA CAGCCCCTGC 3210 GTGCGTAGGG CACGCATCCC 3390 TGGGGGATTT GTCGGGGACG 3030 CCCAGGGTGA CGAGGGGCCC AGCGCTGCCC TCGCGACGGG GGGTCCCACT GCTCCCCGGG 2850 GGGTGCTCGG CCCACGAGCC ATGGGGGACAC GTTCAACAAA CTGCACAGCA GACGIGICGI GGATCAGGTA CAAGITGITT 3470 3290 TACCCCTGTG 3380 3560 GAGCCGTCCC Crercrerer 3200 CCTAGTCCAT CTCGGCAGGG 3110 GACAGACACA 3020 TAAAGCACCC ATTTCGTGGG 2930 GAGGCAGAGC CTCCGTCTCG GCAAGCCCCC 2840 CGTTCGGGGG CACCTCAAGG GTGGAGTTCC CCCGGGCGAA TCGCACCCGC GCCCAGACCC CGGGTCTGGG GGGCCCGCTT GCCCCCGTAC AGCGTGGGCG AGCCCCTGGG CGGGGGCATG 3280 TCCCCGACGG 3190 3370 AGGGGCTGCC TCGGGGACCC TCGTACCITT TGGCATGAGG ACCGTACTCC 3010 AGCATGGAAA 3100 GCGACGGCCG 2920 CGCTGCCGGC 2830 CCCCACGCGG GGGGTGCGCC CTGCCCAGCC GACGGGTCGG CACACACTCA GTGTGTGAGT 3450 CGGAGCCTCA GCCTCGGAGT 3360 CATGCCCACT GTACGGGTGA 3270 CCCGAGTCGG AAGCCCTAGG TTCGGGATCC GGGCTCAGCC CTCCGGACTC GAGGCCTGAG 3180 CCGGGCGCCC 0000000000 2910 3000 3090 GTAAATGAGT CATTTACTCA 2820 CCCCCACGAG GGGGGTGCTC GATGCCCACA CGGAGTGTGT CCTGGCTGCC GGACCGACGG CTACGGGTGT 3440 GCCTCACACA 3260 3350 TCCCGACCTC AGGGCTGGAG GGGCCACGGG 3170 GGGATCCCAC CCCGGTGCCC CCGGCTCAGA 2990 CCCTAGGGTG 3080 TACATACTIC GGCCGAGTCT ATGTATGAAG CTGTCTCCGG GACAGAGGCC CGGACACAGG GCCTGTGTCC CCGTGATTGG GACTGGTGCA ACACGTGCAC TGTGCACGTG GGCACTAACC CTGACCACGT 3430 GCCCTGTCC CGGGGACAGG 3340 gcccraager CGGGACCCGA ACGGACCCGG 3070 GTACCCCCTG CCACGGGTCA GGTGCCCAGT receredence CATGGGGGAC GAGCCTCTCC CTCGGAGAGG

ATTGGCAAGA

TAACCGTTCT

TTTATACCCC

AAATATGGGG

CCGTGTCCCA GGCACAGGGT

TGCATCGTCG

AGTACCAAGC TGGTAACTTG ACGTAGCAGC

ACCATTGAAC

TCATGGTTCG

GGGCGACGGT

CCCGCTGCCA

GGATTTTATC CCTAAAATAG

AAGGCTGGTA TTCCGACCAT

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## FIG. 14E

Primary Sequence = SEQ ID NO:10

Complementary Sequence = SEQ ID NO:28 TCCTAGCGTG AGGATCGCAC AAGTAGTGAG CGATAAGGTC TTCATCACTC 4230 CCCAGTTCCG GGATTGAGGC GGGTCAAGGC 3870 CATTCTATTC 3960 ATGGCTTCTG TACCGAAGAC GTTACGCGCA CAATGCGCGT CCTCTCAAAA GGAGAGTTTT GTAAGATAAG CCCGTGCCTT TGGCCCACTT ACCEGETGAA GGGCACGGAA AACTGCCGTT GCTATTCCAG TIGACGGCAA CCTAACTCCG CCCACACCAC GTTCGCCGGG GGGTGTGGTG CANGCGGCCC GGTGGGCTCT CCACCCGAGA GAGTAGGTGT CTCATCCACA 3950 TECCCCTCC AGGGACCGGG GTAGACAACA AACGGGGAGG TCCCTGGCCC 3860 CGCGCCAAAC GCGCGGTTTG CGGCCTCTGA GCCGGAGACT TTCTCGCCAC 4210 CCATCCCGCC GGTAGGGCGG 4120 AAAGCGAAAG AAGCGAAGGA AAGAGCGGTG CGCATTGTCT CITTAACGTA GCGTAACAGA CTGGGGATGC GACCCCTACG TAAGCGCGGC ATTCGCGCCG GGTGCAGTGC 3940 CATCTGTTGT 3850 4030 CCACGTCACG 3760 3670 GCTGCGATTT CTCCGGCGGA 4380 CGACGCTAAA GAGGCCGCCT CTAACTCCGC AGCGGCGCAT TCGCCGCGTA TICCCTICCT 4200 TCAGGGCGGG GATTGAGGCG 4290 4110 AGCAGGCATG TCGTCCGTAC GAMATTGCAT 4020 AGTTGCCAGC GICGGAGCIG ACACGGAAGA ICAACGGICG 3930 CCTAGIGIGI 3840 GGATCACACA ACAGCTCAGG TGTCGAGTCC TGCAGAGGCC ACGICICCGG AGTCCCGCCC TITCGCTITC 4370 CGCGCCCTGT GCGCGGGACA 4190 GGAAGACAAT CCTTCTGTTA 4010 4100 ATAAAATGAG TATTTACTC 3920 TGTGCCTTCT 3830 GTGTGTGTCC CACACACAGG 3740 AAAAGCTTGG GICCITIGGIA TTTTTTTT CGGGGTACCG ACTGATTAAA AAAATTAAAT TTTTCGAACC CAGCAACCAT GCGGGCGAGG 4180 4270 CCCTCCTAAC CGCCCGCTCC GGGAGGATTG GGTATCCCCA CCATAGGGGT 4090 TCCTTTCCTA AGGAAAGGAT 3910 CAGCCTCGAC AGCCGCCACA TCGGCGGTGT 3820 GGCTTTTGCA CCGAAAACGT GCCCCATGGC TGACTAATTT CTCAATTAGT 4350 TCGCGGGATC 4170 GAGTTAATCA 4260 AGCGCCCTAG GGCTCTAGGG CCGAGATCCC CAGGACGGAT ACTCCCACTG TGAGGGTGAC GACAGCAAGG CTGTCGTTCC 3900 3990 Grececree CACGGGGACG GTCCTGCCTA 3810 TGGAGGCCTA AAGCATGCAT ACCTCCGGAT TTCGTACGTA TACACTTGCC 4340 GGTGGGGCAG ATGTGAACGG 4160 CCTTCCACGG CCACCCGTC AACCAGCTGG TTGGTCGACC GGGAAGGGAC GGAAGGTGCC 4070 CCCTTCCCTG TCTCACAAGG GGTCGGGAGG AGAGTGTTCC GAGGCTTTTT CTCCGAAAAA AAGGGAAAAA TTCCCTTTTT CCCATTCTCC GGGTAAGAGG GCGTGACCGC CGCACTGGCG AGGCGGAAAG TCCGCCTTTC CCTTGACCCT GGAACTGGGA TGGGGGGTGG ACCCCCCACC CCCAGTGCCG GGGTCACGGC CCAGCCCTCC

## FIG. 14F Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

4860

4850

4840

4830

4820

4810

GCAAGTAAAG

4760

4750

4740

TTATTGAACA ACCGGAATTG

GCCTTAAGAC

TTTGGATGAT

TIGCCAAAG

GCTCATTTC

TGGTGCTCCT

AGTITCTIGG

TCAAAGAACC

4690

ACCACGAGGA

4710

TGGCCTTAAC

AATAACTTGT

CGAGTAAAAG AACGGTTTTC AAACCTACTA CGGAATTCTG

ACAAGGATCA TGTTCCTAGT

ACTCTTTGTG

GCCACCTTAG

AATCAACCAG TTAGTTGGTC

GGAAGCCATG

CCTTCGGTAC

CTGTTTACCA

CCTCCGTCAA

GGAGGCAGTT

TTGGATAGTC AACCTATCAG

ATCTGTACCA

TAGACATGGT

4790

CGGTGGAATC

TGAGAAACAC

CTCTCTGAGG

CCCAGGCGTC

TCCCAGAATA

ATATTTGAAG

TATABACTIC

TTTGGGGAAA

CAGAAATTGA GTCTTTAACT

TGCARAAAGG

ACGITITICC

TGAAAGTGAC ACTTTCACTG

ACGICCITAA

TGCAGGAATT

4880

4920

4910

4900

4890

4940

5040

GCTCCCCTCC

GTTCAAGAGA

CAAGITCICI

AAGATGCTTT

GACTAACAGG

CGAGAAGAAA

TTGAAGTCTA

AAGTATAAGT

AAAAGGCATC

TCCAGGAGGA

TITICCGIAG

4990

TTCATATTCA AACTTCAGAT

CTGATTGTCC

5020

5010

5000

5130

5120

5110

5100

5090

5080

5070

TGACATAATT

TTCTGTGGTG

GGAACCTTAC

TCTTTGTGAA

GCTTTAGATC

ACTITIGCIG

AGACCATGGG

CATTTTATA

TAAAGCTATG

AGGACTITCC TCCTGAAAGG ATTAACAAAC TAATTGTTTG CAGAAGAAAT GICTICTITA AAGACACCAC ACTGTATTAA GAAGACCCCA CITCIGGGGT GATGACTAAG GACAAAACGA CTACTGATTC 5300 CIGITITICI 5390 5210 ACTCCTTTTG GAGAAAGGTA CTCTTTCCAT TGAGGAAAAC 5380 CCTTGGAATG ATGTGTTAAA TACACAATIT 5200 GTTTTTCTT CAAAAAAGAA TAAGTGTATA TACGGAAATT ATTCACATAT ATGCCTTTAA 5370 5190 CGAAATCTAG AGAAACACTT GAGAGITGIA AGAIGAGGAG GGATGICICI AAATITICGAG AITCCAITIA TATITIAAA 5360 TCTACTCCTC ATAAAATTT CAGTGGTGGA GTCACCACCT 5270 5180 CTCTCAACAT TGAATGGGAG ACTTACCCTC TAAGGINAAT TGAAAACGAC 5260 5170 GATGACGACT CTACTGCTGA ATGGAACTGA TACCTIGACT TTTAAAGCTC 5160 TCTGGTACCC CGGTAGATCA CTACTACTCC GATGATGAGG ATTCCAACCT TAAGGTTGGA CCTACAGAGA GTAAAAATAT 5240 GCCATCTAGT ACATABAATC IGTATTTAG CCIGITIGAL GGACAAACTA ATTTCGATAC

pD17-cJ-dCH2.H1

AAACAGAATC

AGTGGAAGGT

GTTGGAGAAG

CATGAAGGTT TCTTACTGGT

CAACCTCTTC

AGAATGACCA

GTACTTCCAA

ACCAGTTCAA

GGCGAGTCCT

TGCCTCTGGA TGGGACCGGA

CCGCTCAGGA

ACCCTGGCCT

ACGGAGACCT

4570

TITGICTIAG

TATAGETICEC AGTAGAGAAC ATATCAAGAG TCATCTECTEG

TGTCTTAATT

ACAGAATTAA

CCTTTAAAGG

4650

GGAMATTTCC

CITCTIAGCT

4640 GAAGAATCGA

CCATTCCTGA

ACCTGGTTCT

TGGACCAAGA

CCCATCCTTT

TGGTGATTAT

GGGTAGGAAA

4600

4630

GGTAAGGACT

## FIG. 14G Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

5760

5750

5740

5730

5720

TTAATAAGGA

TGTAAAGGGG

CITITIAATT

GTACCTTTAG

CAAAAATTGT

5640

5630

5620

GAAAATTAA ACATTTCCCC

GITITIAACA CAIGGAAATC

ATTGATACGA

TAACTATGCT

CTGCTATTAA

GTATCTCACA

CATAGAGTGT

TCCACACAGG

5600

AATTATTCCT

CTCCCACACC

TTTAAAAAC

TTTTACTTGC

TTTGTAGAGG

CCATACCACA

TCATAATCAG

ATATCACGGA ACTGATCTCT AGTATTAGTC

TGACTAGAGA

TATAGTGCCT

TATAAACTAC

ATATTTGATG

5700

5690

GGTATGGTGT AAACATCTCC AAAATGAACG AAATTTTTTG

AGCAATAGCA TCGTTATCGT

AATGTTTATT

TTACABATAA

CTTATAATGG

TTTATTGCAG

TGTTAACTTG

5810

5800

5790

5780

ACAATTGAAC AAATAACGTC

GITTAACAACA

CAATTGTTGT

AAAATGAATG TTTTACTTAC

CCTGAAACAT

TCCCCCTGAA

GGACTTTGTA

5830

5820

5940

GTCTGGATCG

ATCTTATCAT TAGAATAGTA

TCATCAATGT AGTAGTTACA

AACAGGTTTG

ATCAACACCA

CACTGCATIC 1

TAGTTGTGGT

5900

5890

5880

GCATTITITI

CACAAATAAA

TCACAAATTT

TTGTCCAAAC

5910

5920

6030

6020

6010

6000

5990

5980

TACAAATAAA

TTATAATGGT

TTATTGCAGC

CCCAACTIGT

CTTCGCCCAC

TGCTGGAGTT

GGGGATCTCA

CCTCCAGCGC

GCTGGATGAT

5960

AGTGACGGGC TCAACACCAA ACAGGTTTGA GTAGTTACAT AGAATAGTAC ACAATTCCAC TGTTAAGGTG TCACTGCCCG GGGTTGAACA AATAACGTCG AATATTACCA ATGTTTATTT TCTTATCATG CACTCGATTG AGTGTAATTA ACGCAACGCG TTATCCGCTC ACACTTTAAC AATAGGCGAG CATCAATGIA TGCGTTGCGC 6110 GIGAGCIAAC ICACATIAAI TGTGAAATTG TGTCCAPACT 6280 6100 GACAAAGGAC CATITITIC ACTGCATICT AGTIGIGGTI CTGTTTCCTG 6270 0609 6180 TGCCTAATGA GTAAAAAAG TGACGTAAGA TGGCGTAATC ATGGTCATAG TACCAGTATC TOTTGIATGC TCGGCCTTCG TATTICACAT TTCGGACCCC ACGGATTACT GAAGCGGGTG 6080 6170 ACAACATACG AGCCGGAAGC ATAAAGTGTA AAGCCTGGGG ACCGCATTAG 6250 ACGACCTCAA 6160 6070 CAGCTGGAGA TCGATCTCGA AGCTAGAGCT ACAAATAAAG TGTTTATTTC 6150 CCCCTAGAGT 0909 Gregacerer 6230 CACAAATTTC GTGTTTAAG GGAGGTCGCG 6140 AGACATATGG ICTGIAIACC GCAATAGCAT CGTTATCGTA CGACCTACTA

pD17-cJ-dCH2.H1

AAAAGCTGC

ACCACAAAGG

TGCTATTTAC

TIGCTIGCTI

AATAGAACTC

TGTGTTTAGT

5440

GATTCAAAAA ACTCAGTACG ACACAAATCA

TGAGTCATGC

CIRAGITITI

TTCAGAATTG AAGTCTTAAC

5460

TTATCTTGAG AACGAACGAA ACGATAAATG TGGTGTTTCC

TTTTCGACG

TITITITAC

AACATACTGT

TTATAATCAT

GGCATAACAG

5560

TTGTATGACA AAAAAGAATG

CCGTATTGTC AATATTAGTA

AAATATTCAT

TGACGATATG TTCTTTTAAT ACCTTTTTAT AAGACATTGG

TTTATA TTA

TTCTGTAACC

TGGAAAATA

AAGAAAATTA

ACTGCTATAC

5520

5510

5540

5530

**FIG. 14H** Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

TITITCCIAG AGTICITCIA GGAAACTAGA AAAGAIGCCC CAGACIGCGA GICACCIIGC CAGTGGAACG 7110 GTATTTGGTA CCACCAAAAA 6840 6930 CATAAACCAT GGTGGTTTTT 6750 GGAAGCGTGG CCTTCGCACC CCCGTTCAGC GGGCAAGTCG ACTGGTAACA TGACCATTGI 9999 TACCAGGCGT 6570 TTATCCACAG AATAGGTGTC GCGTTTTCC CGCHARAAGG ATGGTCCGCA GCGAGAAGGC GTCTGACGCT TAGAAGGACA CGCTGGTAGC GCGACCATCG GGCAGCAGCC CCGTCGTCGG ATCTTCCTGT GCACGAACCC TCTCCCTTCG TGGCCTATGG ACAGGCGGAA AGAGGGAAGC CGTGCTTGGG ACTATAAAGA TGATATTTCT CGCGTTGCTG GCGCAACGAC CCATTATGCC CGCATAACCC GGTAATACGG 6470 TTTCTACGGG AACAAACCAC TGCCGATGTG 7180 ACGGCTACAC 7090 TTGTTTGGTG TATCGCCACT ATAGCGGTGA TGTCCGCCTT TGGGCTGTGT ACCCGACACA 6910 ACCCGACAGG TGGGCTGTCC 6730 6820 GTAAAAAGGC CATITITICG 6640 ACTCAAAGGC CTCCGCCAAA TGAGTTTCCG 6460 7170 CCTTTGATCT TGATCCGGCA AGACACGACT TCTGTGCTGA TGGCCTAACT ACCEGATTGA 7080 ACTAGGCCGT CGCTCCAAGC GCGAGGTTCG 6990 ACCEGATACE AGGTGGCGAA TCCACCGCTT 6810 6900 GTATCAGCTC CATAGTCGAG GCCAGGAACC CGGTCCTTGG 6450 6540 6630 GCGCGCCCT AAAAAGGATC TCAAGAAGAT TGGTAGCTCT CITITICICA ACCATCGAGA 7160 GTTGGGCCAT GAACTTCACC CAACCCGGTA 6980 CTTGAAGTGG 7070 CCTGCCGCTT GGACGCCGAA GTAGGTCGTT CATCCAGCAA 6890 CTCAAGTCAG 6800 GAGTTCAGTC GCGGCGAGCG CGCCGCTCGC CCAGCAAAAG GGTCGTTTTC 6620 6440 6530 TTAGCCGGTT 7150 GATGTCTCAA GAAAAAGAGT 7060 GICITGAGIC CAGAACTCAG CTACAGAGTT AGTCAAGCCA 6970 6790 TCAGTTCGGT 6980 CTGTTCCGAC GACAAGGCTG 6610 AAAATCGACG TTTTAGCTGC GAGCAAAAGG CTCGTTTTCC AGCAAGCCGA ACGTAATTAC 6430 TCGTTCGGCT 6520 ACGCGCAGAA CGTCGTCTAA TGCGCGTCTT GTTACCTTCG 7140 CATCCGCCAC CAATGGAAGC ACATCCATAG GGTAACTATC GTAGGCGGTG 7050 CCATTGATAG 6699 6780 TGTAGGTATC 969 GAGCATCACA GIGCGCICIC CACGCGAGAG CTCGTAGTGT AAGAACATGT TTCTTGTACA AGCACGCTCG GACGCGAGCC 6600 CTGCGCTCGG 6510 6420 GCAGCAGATT GCTGAAGCCA 7130 CGACTTCGGT 6950 AGCGAGGTAT TCGCTCCATA 7040 CGCCTTATCC GCGGAATAGG ATGCTCACGC TACGAGTGCG 0989 AAGCTCCCTC TAACGCAGGA CCCCCCTGAC GGGGGGACTG TTCGAGGGAG ATTGCGTCCT 6590 GTGACTGAGC CCCTTTGGAC CACTGACTCG 6410 AGACGCGAGA TTGTTTGCAA AACAAACGTT GGATTAGCAG CCTAATCGTC TCTGCGCTCT CCGACCGCTG GGCTGGCGAC Treceered CGCTTTCTCA GCGAAAGAGT AAGGGGGACC TATCCGAGGC ATAGGCTCCG GAAGGAGCGA AATCAGGGA TTAGTCCCCT GAAAGGTCAG CTTCCTCGCT

pD17-cJ-dCH2.H1

CGCTCTTCCG

GCGTATTGGG

GAGGCGGTTT

CGCGCGGGGA

AATCGGCCAA

TGCATTAATG

TCGTGCCAGC

GGGAAACCTG

CTTTCCAGTC

6340

6330

6360

CTTTTGAGAG

#### 20/53

FIG. 14I

Primary Sequence = SEQ ID NO:10 Complementary Sequence = SEQ ID NO:28

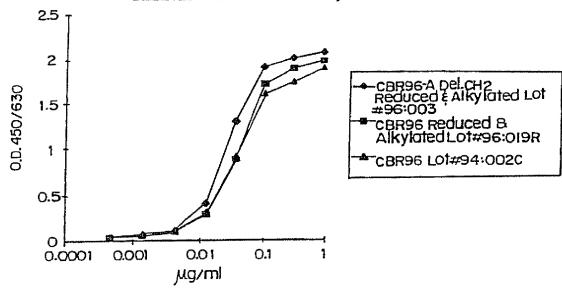
8010 TTTACTTTCA GGTTGACTAG AAGTCGTAGA AAATGAAAGT CGGCGACCGA ACCTITIGGA AGNAGCCCCG TCTTCGGGGC 7740 7560 ACAGGCATCG TTGTGCAAAA CIGCALAALT GACGTATTAA GCCGCTGGCI AACACGITIT TCCGCCTCCA TGTCCGTAGC AGGCCCAGGT TITCGLICAL CCGCGAGACC GGCGCTCTGG **AAAGCAAGTA** TITABATCAR TITIACTICA AAAITIAGII TGGAAAACGT TTCAGCATCT ATAGTGTATG TATCACATAC TATGGCAGCA TGCCATTGCT CGTTGCAACA ACGGTAACGA ATCCCCCATG TAGGGGGTAC ATACCGTCGT B000 CTAGACAGAT TGCAACTTTA ACGTTGAAAT TGCAATGATA 7730 GATCIGICIA ACGITACTAT AAAATGAAGT 7370 TGCTCATCAT CCAACTGATC CACTCATGGT 8080 GAGTTACATG GTGAGTACCA CATTCTGAGA 7990 ACGAGTAGTA CTCAATGTAC GTAAGACTCT GCAACGTTGT CTTCACCAGG 7720 GCCCCAGTGC 7540 GAAGTGGTCC CTATCTCAGC GATAGAGTCG CGGGGTCACG TTTAAATTA 7450 AAATTTAAT 7270 7360 ACTCGTGCAC TGAGCACGTG ACTITARAG TGAAATTTTC CGTCACAATA TCAACCAAGT AGTIGGTICA GCAGTGTTAT 8070 CGATCAAGGC GCTAGTTCCG AATAGTTTGC TTATCAAACG 7800 7890 TTACCATCTG 7530 GCCGAGCGCA CGGCTCGCGT 7620 7710 AATGGTAGAC 7350 ATGCTTAATC AGTGAGGCAC TACGAATTAG TCACTCCGTG 7440 ACCTAGATCC TGGATCTAGG 7260 GATGTAACCC CTACATTGGG ACATAGCAGA TGTATCGTCT ACCACTCATG 7970 8060 GCCAAGGGTT TAAGTTGGCC ATTCAACCGG 7880 TGGTGAGTAC CGGTTCCCAA TGCCCTCCCG TTCGCCAGTT AAGCGGTCAA 7700 AGCCGGAAGG TCGGCCTTCC AAGGATCTTC TAACTACGAT ACGGGAGGGC 7610 7790 TTCCTAGAAG 7430 7340 7250 CTAGGTCAAG GATCCAGTTC AACAGICTIC AAAGACACTG ATACCGCGCC TATGGCGCGG 8050 TTTCTGTGAC 7960 TTGTCAGAAG CATTCAGCTC 7780 ATTGATGCTA TAAACCAGCC GAGTAAGTAG CTCATTCATC 7690 GTAAGTCGAG 7870 ATTTGGTCGG ACAGTTACCA TGTCAATGGT 7510 GATTATCAAA CTAATAGTTT 7330 7420 GGCGACAACT CCGCTGTTGA ATACGGGATA TATGCCCTAT GGAGGCTAGC CATTCTACGA 8040 7950 7860 GTAAGATGCT GGTATGGCTT CCATACCGAA 7770 CCTCCGATCG TTATCAGCAA CGGGAAGCTA GCCCTTCGAT CAGCACATCT GTCGTGTAGA 7500 AATAGTCGTT ACTTGGTCTG TGAACCAGAC 7320 7410 TTGGTCATGA AACCAGTACT AAGGATCTTA TTCCTAGAAT CCCGGCGTCA CATGCCATCC GGGCCGCAGT GTACGGTAGG CTCCTTCGGT GAGGAAGCCA 7940 CCGAGGTCTA CICGICGITI GGCTCCAGAT 7580 TAATTGTTGC ATTAACAACG GAGCAGCAAA 7850 TATACTCATT CTGACTCCCC GACTGAGGGG 7490 AATTCCCTAA ATATGAGTAA TIAAGGGATI 7310 GAMACTCTC CAACGAGAAC GTTGCTCTTG CTCTTACTGT Tredecaare GAGAATGACA TCCAGTCTAT AAGCGGTTAG TGGTGTCACG ACCACAGTGC GTGCGAGTGG AGGICAGATA CCATAGTTGC GGTATCAACG CACGCTCACC AGATTTCATA AAAACTCACG TCTAAAGTAT TTTTGAGTGC

FIG. 14J
Primary Sequence = SEQ ID NO:10
Complementary Sequence = SEQ ID NO:28

8190 CTCATACTCT GAGTATGAGA	8280 AAACAAATAG TTTGTTTATC	
8180 ATGTTGAATA TACAACTTAT	8270 TTAGAAAAT AATCTTTTA	
8170 CGACACGGAA GCTGTGCCTT	8260 TTGAATGTAT AACTTACATA	
B160 GGAATAAGGG CCTTATTCCC	8250 GGATACATAT CCTATGTATA	
8150 CGCAAAAAA GCGTTTTTC	8240 TCTCATGAGC AGAGTACTCG	8330 C G
8140 GGCAAAATGC CCGTTTTACG	8230 AGGGTTATTG TCCCAATAAC	8320 CACCTGACGT GTGGACTGCA
8110 8120 8130 8140 8150 8150 8150 8150 8170 8190 8190 8190 8190 8190 8190 8190 819	8280 8250 8250 8280 8280 8280 8280 8280	8290 8320 8320 8310 8320 CACCTGACGT CCCCAAGGCGC GTGTAAAGGG GCTTTTCACG GTGGACTGCA G
8120 TGGGTGAGCA ACCCACTCGT	8210 ATATTATTGA TATAATAACT	8300 CACATTICCC GTGTAAAGGG
8110 CCAGCGTTTC GGTCGCAAAG	8200 TCCTTTTTCA AGGAAAAAGT	8290 GGGTTCCGCG CCCAAGGCGC

FIG. 15

## COMPARISON OF WHOLE CHIBR96 AND DELETED CH2 CHIBR96 ON LEY/K ELISA



## FIG. 16

hBR96-2B:L235 to A235 and G237 to A237

hBR96-2C:E318 to S318, K320 to S320, and K322 to S322

hBR96-2D:P331 to A331

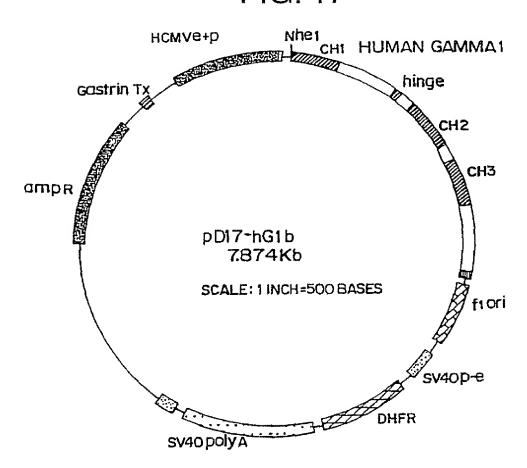
hBR96-2E:L235 to A235, G237 to A237, E318 to S318, K320 to S320, and K322 to S322

hBR96-2F:L235 to A235, G237 to A237, and P331 to A331

hBR96-2G:E318 to S318, K320 to S320, K322 to S322, and P331 to A331

hBR96-2H: L235 to A235, G237 to A237, E318 to S318, K320 to S320, K322 to S322, and P331 to A331

FIG. 17



## FIG. 18A

(SEQ ID NO:22)

	<b>,</b>			
1 GGTACCAA	ATADITAAAT TT	TCTCCTTAGG	TCTCGAGTCT	CTAGATAACC
51 GGTCAATC	ga tiggaatict	TGCGGCCGCT	TGCTAGCCAC	CATGGAGTTG
101 TGGTTAAG	CT TGGTCTTCCT	TGTCCTTGTT	TTAAAAGGTG	TCCAGTGTGA
151 AGTGCAAC	ig giggagicig	GGGGAGGCTT	AGTGCAGCCT	GGAGGGTCCC
201 TGCGACTT	TC CTGTGCTGCA	TCTGGATTCC	CETTCAGTGA	CTATTACATG
251 TATTGGGT	rc gccaggcicc	AGGCAAGGGA	CTGGAGTGGG	TCTCATACAT
301 TAGTCAAG	at ggtgat <b>a</b> taa	CCGACTATGC	AGACTCCGTA	AAGGGTCGAT
351 TCACCATC	TC CAGAGACAAT	GCAAAGAACA	GCCTGTACCT	GCAAATGAAC
401 AGCCTGAGG	eg acgaggacac	agccgtgtat	TACTGTGCAA	GAGGCCTGGC
451 GGACGGGG	C TGGTTTGCTT	ACTGGGGCCA	AGGGACTCTG	GTCACGGTCT
501 CTTCCGCT	G CACCAAGGGC	CCATCGGTCT	TCCCCCTGGC	ACCCTCCTCC
551 AAGAGCACO	T CTGGGGGCAC	AGCGGCCCTG	GGCTGCCTGG	TCAAGGACTA
601 CTTCCCCGA	A CCGGTGACGG	TGTCGTGGAA	CTCAGGCGCC	CTGACCAGCG
651 GCGTGCACA	CITCCCGCT	GTCCTACAGT	CCTCAGGACT	CTACTCCCTC
701 AGCAGCGTG	G TCACCGTGCC	CTCCAGCAGC	TYGGGCACCC	AGACCIACAT
751 CTGCAACGT	G AATCACAAGC	CCAGCAACAC	CAAGGTGGAC	AAGAAAGTTG
801 GTGAGAGGC	C AGCACAGGGA	GGGAGGGTGT	CTGCTGGAAG	CCAGGCTCAG
851 CGCTCCTGC	C TGGACGCATC	CCGGCTATGC	AGCCCCAGTC	CAGGGCAGCA
901 AGGCAGGCC	c cercrecere	TTCACCCGGA	GCCTCTGCC	CGCCCCACTC
951 ATGCTCAGG	G AGAGGGTCTT	CIGGCITTII	CCCCAGGCTC	TGGGCAGGCA
1001 CAGGCTAGG	T GCCCCTAACC	CAGGCCCTGC	ACACAAAGGG	GCAGGTGCTG
1051 GGCTCAGAC	C TGCCAAGAGC	CATATCCGGG	AGGACCCTGC	CCCTGACCTA
1101 AGCCCACCC	C AAAGGCCAAA	CTCTCCACTC	CCTCAGCTCG	GACACCTTCT
1151 CTCCTCCCAC	G ATTCCAGTAA	CTCCCAATCT	TETETETECA	GAGCCCAAAT
1201 CTTGTGACA	A AACTCACACA	TGCCCACCGT	GCCCAGGTAA	GCCAGCCCAG
1251 GCCTCGCCC	r ccasctcaag	GCGGGACAGG	TGCCCTAGAG	TAGCCTGCAT
1301 CCAGGGACAG	GCCCCAGCCG	GGTGCTGACA	CGTCCACCTC	CATCTCTTCC

#### FIG. 18B (SEQ ID NO:22) 235 237

		235	237		
1351	TCAGCACCTG	AACTCCTGGG	GGGACCGTCA	GTCTTCCTCT	TCCCCCAAA
1401	ACCCAAGGAC	ACCCTCATGA	TCTCCCGGAC	CCCTGAGGTC	ACATGCGTGG
1451	TGGTGGACGT	GAGCCACGAA	GACCCTGAGG	TCAAGTTCAA	CTGGTACGTG
1501	GACGGCGTGG	AGGTGCATAA	TGCCAAGACA	AAGCCGCGGG	AGGAGCAGTA
1551	CAACAGCACG	TACCGTGTGG	TCAGCGTCCT	CACCGTCCTG	CACCAGGACT
		318	320 322		
1601	GGCTGAATGG	CAAGGAGTAC	AAGTGCAAGG	TCTCCAACAA	AGCCCTCCCA
1651	331 GCCCCCATCG	AGAAAACCAT	CTCCAAAGCC	aaaggtggga	CCCGTGGGGT
1701	GCGAGGGCCA	CATGGACAGA	GCCCGCTCG	GCCCACCCTC	TGCCCTGAGA
1751	GTGACCGCTG	TACCAACCTC	TGTCCCTACA	GGGCAGCCCC	GAGAACCACA
1801	GGTGTACACC	CTGCCCCCAT	CCCGGGATGA	GCTGACCAAG	AACCAGGTCA
1851	GCCTGACCTG	CCTGGTCAAA	GGCTTCTATC	CCAGCGACAT	CGCCGTGGAG
1901	TGGGAGAGCA	ATGGGCAGCC	GGAGAACAAC	TACAAGACCA	CGCCTCCCGT
1951	GCTGGACTCC	GACGGCTCCT	TCTTCCTCTA	CAGCAAGCTC	ACCGTGGACA
2001	AGAGCAGGTG	GCAGCAGGGG	AACGTCTTCT	CATGCTCCGT	GATGCATGAG
2051	GCTCTGCACA	ACCACTACAC	GCAGAAGAGC	CTCTCCCTGT	CTCCGGGTAA
2101	ATGAGTGCGA	CGGCCGGCAA	GCCCCCGCTC	CCCGGGCTCT	CGCGGTCGCA
2151	CGAGGATGCT	TGGCACGTAC	CCCCTGTACA	TACTTCCCGG	GCGCCCAGCA
2201	TGGAAATAAA	GCACCCAGCG	CTGCCCTGGG	CCCCTGCGAG	ACTGTGATGG
2251	TTCTTTCCAC	GGGTCAGGCC	GAGTCTGAGG	CCTGAGTGGC	ATGAGGGAGG
2301	CAGAGCGGGT	CCCACTGTCC	CCACACTGGC	CCAGGCTGTG	CAGGTGTGCC
2351	TGGGCCCCCT	AGGGTGGGC	TCAGCCAGGG	GCTGCCCTCG	GCAGGGTGGG
2401	GGATTIGCCA	GCGTGGCCCT	CCCTCCAGCA	GCACCTGCCC	TGGGCTGGGC
2451	CACGGGAAGC	CCTAGGAGCC	CCTGGGGACA	GACACACAGC	CCCTGCCTCT
2501	GTAGGAGACT	GTCCTGTTCT	GTGAGCGCCC	CTGTCCTCCC	GACCTCCATG
2551	CCCACTCGGG	GGCATGCCTA	GTCCATGTGC	GTAGGGACAG	GCCCTCCCTC
2601	ACCCATCTAC	CCCCACGGCA	CTAACCCCTG	GCTGCCCTGC	CCAGCCTCGC
2651	ACCCGCATGG	GGACACAACC	GACTCCGGGG	ACATGCACTC	TCGGGCCCTG
2701	TGGAGGGACT	GGTGCAGATG	CCCACACACA	CACTCAGCCC	AGACCCGTTC
2751	AACAAACCCC	GCACTGAGGT	TGGCCGGCCA	CACGGCCACC	ACACACACAC
2801	GTGCACGCCT	CACACACGGA	GCCTCACCCG	GGCGAACTGC	ACAGCACCCA

### FIG. 18C

(SEQ ID NO:22) 2851 GACCAGAGCA AGGTCCTCGC ACACGTGAAC **ACTCCTCGGA** CACAGGCCCC 2901 CACGAGCCCC ACGCGGCACC TCAAGGCCCA CGAGCCTCTC GGCAGCITCT 2951 CCACATGCTG ACCIGCICAG ACAAACCCAG CCCTCCTCTC ACAAGGGTGC 3001 CCCTGCAGCC GCCACACACA CACAGGGGAT CACACACCAC GTCACGTCCC 3051 TGGCCCTGGC CCACTTCCCA GTGCCGCCCT TCCCTGCAGG ACGGATCAGC 3101 CTCGACTGTG CCTTCTAGTT GCCAGCCATC TGTTGTTTGC CCCTCCCCCG 3151 TGCCTTCCTT GACCCTGGAA GGTGCCACTC CCACTGTCCT TTCCTAATAA 3201 AATGAGGAAA TIGCATCGCA TIGICIGAGI AGGTGTCATT CTATTCTGGG 3251 GGGTGGGGTG **GGGCAGGACA GCAAGGGGGA GGATTGGGAA** GACAATAGCA 3301 GGCATGCTGG GGATGCGGTG **GGCTCTATGG** CTTCTGAGGC **GGAAAGAACC** 3351 AGCTGGGGCT CTAGGGGGTA TCCCCACGCG CCCTGTAGCG **GCGCATTAAG** 3401 CGCGGCGGGT **GTGGTGGTTA** CGCGCAGCGT GACCGCTACA CITGCCAGCG 3451 CCCTAGCGCC CGCTCCTTTC GCTTTCTTCC CITCCITICI CGCCACGITC 3501 GCCGGGCCTC TCAAAAAAGG GAAAAAAAGC **ATGCATCTCA** ATTAGTCAGC 3551 AACCATAGTC CCGCCCTAA CTCCGCCCAT CCCGCCCCTA ACTCCGCCCA 3601 GTTCCGCCCA TTCTCCGCCC CATGGCTGAC TAATITITIT TATTTATGCA 3651 GAGGCCGAGG CCGCCTCGGC CTCTGAGCTA TTCCAGAAGT **AGTGAGGAGG** 3701 CITTITIGGA GGCCTAGGCT TTTGCAAAAA **GCTTGGACAG** CTCAGGGCTG 3751 CGATTTCGCG CCAAACTTGA CGGCAATCCT AGCGTGAAGG CIGGIAGGAT 3801 TITATCCCCG CIGCCATCAT GGTTCGACCA TIGAACIGCA TCGTCGCCGT 3851 GTCCCAAAAT ATGGGGATTG GCAAGAACGG AGACCTACCC TGGCCTCCGC 3901 TCAGGAACGA GITCAAGTAC TTCCAAAGAA TGACCACAAC CICITCAGIG 3951 GAAGGTAAAC AGAATCTGGT GATTATGGGT AGGAAAACCT GGTTCTCCAT 4001 TCCTGAGAAG AATCGACCIT TAAAGGACAG AATTAATATA GTTCTCAGTA 4051 GAGAACTCAA AGAACCACCA CGAGGAGCTC ATTITCITGC CAAAAGTTTG 4101 GATGATGCCT TAAGACTTAT TGAACAACCG GAATTGGCAA GTAAAGTAGA 4151 CATGGTTTGG ATAGTCGGAG GCAGITCIGI TTACCAGGAA GCCATGAATC 4201 AACCAGGCCA CCTTAGACTC TTTGTGACAA **GGATCATGCA GGAATTIGAA 4251 AGTGACACGT** TTTTCCCAGA AATTGATTTG **GGGAAATATA** AACTTCTCCC 4301 AGAATACCCA GGCGTCCTCT CIGAGGICCA GGAGGAAAAA **GGCATCAAGT** 

FIG. 18D

4351	ATAAGTTTG!	A AGTCTACGAG	SEQ ID NO:22		A TGCTTTCAAG
4401	TTCTCTGCT	CCCTCCTAA	GCTATGCATT	TTTATAAGAC	CATGGGACTT
4451	TTGCTGGCTT	TAGATCTCTT	TGTGAAGGA	CCTTACTTCT	GTGGTGTGAC
4501	ATAATTGGAC	: AAACTACCTA	CAGAGATTTA	AAGCTCTAAG	GTAAATATAA
4551	AATTTTTAAG	TGTATAATGT	GTTAAACTAC	TGATTCTAAT	TGTTTGTGTA
4601	TTTTAGATTC	CAACCTATGG	AACTGATGAA	TGGGAGCAGT	GGTGGAATGC
4651	CTTTAATGAG	GAAAACCTGT	TTTGCTCAGA	AGAAATGCCA	TCTAGTGATG
4701	ATGAGGCTAC	TGCTGACTCT	CAACATTCTA	CTCCTCCAAA	AAAGAAGAGA
4751	AAGGTAGAAG	ACCCCAAGGA	CTTTCCTTCA	GAATTGCTAA	GTTTTTTGAG
4801	TCATGCTGTG	TTTAGTAATA	GAACTCTTGC	TTGCTTTGCT	ATTTACACCA
4851	CAAAGGAAAA	AGCTGCACTG	CTATACAAGA	AAATTATGGA	AAAATATTCT
4901	GTAACCTTTA	TAAGTAGGCA	TAACAGTTAT	AATCATAACA	TACTGTTTTT
4951	TCTTACTCCA	CACAGGCATA	GAGTGTCTGC	TATTAATAAC	TATGCTCAAA
5001	AATTGTGTAC	CTTTAGCTTT	TTAATTTGTA	AAGGGGTTAA	TAAGGAATAT
5051	TTGATGTATA	GTGCCTTGAC	TAGAGATCAT	AATCAGCCAT	ACCACATTTG
5101	TAGAGGTTTT	ACTTGCTTTA	AAAAACCTCC	CACACCTCCC	CCTGAACCTG
5151	АААСАТАААА	TGAATGCAAT	TGTTGTTGTT	AACTTGTTTA	TTGCAGCTTA
5201	TAATGGTTAC	AAATAAAGCA	ATAGCATCAC	AAATTTCACA	AATAAAGCAT
5251	TTTTTTCACT	GCATTCTAGT	TGTGGTTTGT	CCAAACTCAT	CAATGTATCT
5301	TATCATGTCT	GGATCGGCTG	GATGATCCTC	CAGCGCGGGG	ATCTCATGCT
5351	GGAGTTCTTC	GCCCACCCCA	ACTTGTTTAT	TGCAGCTTAT	AATGGTTACA
5401	AATAAAGCAA	TAGCATCACA	AATTTCACAA	ATAAAGCATT	TTTTTCACTG
5451	CATTCTAGTT	GTGGTTTGTC	CAAACTCATC	AATGTATCTT	ATCATGTCTG
5501	TATACCGTCG	ACCTCTAGCT	AGAGCTTGGC	GTAATCATGG	TCATAGCTGT
5551	TTCCTGTGTG	AAATTGTTAT	CCGCTCACAA	TTCCACACAA	CATACGAGCC
5601	GGAAGCATAA	AGTGTAAAGC	CTGGGGTGCC	TAATGAGTGA	GCTAACTCAC
5651	ATTAATTGCG	TTGCGCTCAC	TGCCCGCTTT	CCAGTCGGGA	AACCTGTCGT
5701	GCCAGCTGCA	TTAATGAATC	GGCCAACGCG	CGGGGAGAGG	CGGTTTGCGT
5751	ATTGGGCGCT	CTTCCGCTTC	CTCGCTCACT	GACTCGCTGC	GCTCGGTCGT
5801	TCGGCTGCGG	CGAGCGGTAT	CAGCTCACTC	AAAGGCGGTA	ATACGGTTAT

## FIG. 18E

		(SEO I	D NO:22)		
5851	CCACAGAATC	AGGGGATAAC	GCAGGAÁAGA	ACATGTGAGC	AAAAGGCCAG
5901	CAAAAGGCCA	GGAACCGTAA	AAAGGCCGCG	TIGCIGGCGI	TITITCCATAG
5951	GCTCCGCCCC	CCTGACGAGC	ATCACAAAAA	TCGACGCTCA	AGTCAGAGGT
6001	GGCGAAACCC	GACAGGACTA	TAAAGATACC	AGGCGTTTCC	CCCTEGAAGC
6051	TCCCTCGTGC	GCTCTCCTGT	TCCGACCCTG	CCGCTTACCG	GATACCTGTC
6101	CGCCTTTCTC	CCTTCGGGAA	GCGTGGCGCT	TTCTCAATGC	TCACGCTGTA
6151	GGTATCTCAG	TTCGGTGTAG	GTCGTTCGCT	CCAAGCTGGG	CTGTGTGCAC
6201	GAACCCCCCG	TTCAGCCCGA	CCGCTGCGCC	TTATCCGGIA	ACTATCGTCT
6251	TGAGTCCAAC	CCGGTAAGAC	ACGACTTATC	GCCACTGGCA	GCAGCCACTG
6301	GTAACAGGAT	TAGCAGAGCG	AGGTATGTAG	GCGGTGCTAC	AGAGTTCITG
6351	AAGTGGTGGC	CTAACTACGG	CTACACTAGA	AGGACAGTAT	TTGGTATCTG
6401	CGCTCTGCTG	AAGCCAGTIA	CCTTCGGAAA	AAGAGTTGGT	AGCTCTTGAT
6451	CCGGCAAACA	AACCACCGCT	GGTAGCGGTG	GITTTITTGT	TTGCAAGCAG
6501	CAGATTACGC	GCAGAAAAAA	AGGATCTCAA	GAAGATCCTT	TGATCTTTTC
6551	TACGGGGTCT	GACGCTCAGT	GGAACGAAAA	CTCACGITAA	GGGATITIGG
6601	TCATGAGATT	ATCAAAAAGG	ATCTTCACCT	AGATCCITIT	AAATTAAAA
6651	TGAAGITITA	AATCAATCTA	AAGTATATAT	GAGTAAACIT	GGTCTGACAG
6701	TTACCAATGC	TTAATCAGTG	AGGCACCTAT	CTCAGCGATC	TGTCTATTTC
6751	GITCATCCAT	AGTTGCCTGA	CTCCCCGTCG	TGTAGATAAC	TACGATACGG
6801	GAGGGCTTAC	CATCTGGCCC	CAGTGCTGCA	ATGATACCGC	GAGACCCACG
6851	CTCACCGGCT	CCAGATTTAT	CAGCAATAAA	CCAGCCAGCC	GGAAGGGCCG
6901	AGCGCAGAAG	TGGTCCTGCA	ACTITATCCG	CCTCCATCCA	GTCTATTAAT
6951	TETTECCEGG	AAGCTAGAGT	aagtagttcg	CCAGTTAATA	GTTTGCGCAA
7001	CGTTGTTGCC	ATTGCTACAG	GCATCGTGGT	GTCACGCTCG	TCGTTTGGTA
7051	TGGCTTCATT	CAGCTCCGGT	TCCCAACGAT	CAAGGCGAGT	TACATGATCC
7101	CCCATGTTGT	GCAAAAAAGC	GGTTAGCTCC	TTCGGTCCTC	CGATCGTTGT
7151	CAGAAGTAAG	TIGGCCGCAG	TGTTATCACT	CATGGTTATG	GCAGCACTGC
7201	ATAATTCTCT	TACTGTCATG	CCATCCGTAA	GATGCTTTTC	TGTGACTGGT
7251	GAGTACTCAA	CCAAGTCATT	CTGAGAATAG	TGTATGCGGC	GACCGAGTTG
7301	CTCTTGCCCG	GCGTCAATAC	GGGATAATAC	CGCGCCACAT	AGCAGAACIT

## FIG. 18F

(SEQ ID NO:22)

		(Did in	1.0.22)		
7351	TAAAAGTGCT	CATCATTGGA	AAACGTTCTT	CGGGGCGAAA	ACTOTCAAGG
7401	ATCTTACCGC	TGTTGAGATC	CAGTTCGATG	TAACCCACTC	GTGCACCCAA
7451	CTGATCTTCA	GCATCTTTTA	CTTTCACCAG	CGTTTCTGGG	TGAGCAAAAA
7501	CAGGAAGGCA	AAATGCCGCA	AAAAAGGGAA	TAAGGGCGAC	ACGGAAATGT
7551	TGAATACTCA	TACTCTTCCT	TITTCAATAT	TATTGAAGCA	TITATCAGGG
7601	TTATTGTCTC	ATGAGCGGAT	ACATATITGA	ATGTATTTAG	AAAAATAAAC
7651	AAATAGGGGT	TCCGCGCACA	TTTCCCCGAA	AAGTGCCACC	TGACGTCGAC
7701	GGATCGGGAG	ATCTGCTAGG	TGACCTGAGG	CGCGCCGGCT	TCGAATAGCC
7751	AGAGTAACCT	TTTTTTTTAA	TITTATTITA	TTTTATTTTT	GAGATGGAGT
7801	TTGGCGCCGA	TCTCCCGATC	CCCTATGGTC	GACTOTCAGT	ACAATCTGCT
7851	CTGATGCCGC	ATAGTTAAGC	CAGTATCTGC	TCCCTGCTTG	TGTGTTGGAG
7901	GTCGCTGAGT	AGTGCGCGAG	CAAAATTIAA	GCTACAACAA	GGCAAGGCTT
7951	GACCGACAAT	TGCATGAAGA	ATCTGCTTAG	GGTTAGGCGT	TITIGCGCTGC
8001	TTCGCGATGT	ACGGGCCAGA	TATACGCGTT	GACATTGATT	ATTGACTAGT
8051	TATTAATAGT	AATCAATTAC	GGGGTCATTA	GTTCATAGCC	CATATATGGA
8101	GTTCCGCGTT	ACATAACTTA	CGGTAAATGG	CCCGCCIGGC	TGACCGCCCA
8151	ACGACCCCCG	CCCATTGACG	TCAATAATGA	CGTATGTTCC	CATAGTAACG
8201	CCAATAGGGA	CTTTCCATTG	ACGTCAATGG	GTGGACTATT	TACGGTAAAC
8251	TGCCCACTTG	GCAGTACATC	aagtgtatca	TATGCCAAGT	ACGCCCCTA
8301	TTGACGTCAA	TGACGGTAAA	TGGCCCGCCT	GGCATTATGC	CCAGTACATG
8351	ACCITATGGG	ACTITICATAC	TIGGCAGTAC	ATCTACGTAT	TAGTCATCGC
8401	TATTACCATG	GTGATGCGGT	TITEGCAGTA	CATCAATGGG	CGTGGATAGC
8451	GGTTTGACTC	ACGGGGATTT	CCAAGTCTCC	ACCCCATTGA	CGTCAATGGG
8501	AGITIGITIT	GGCACCAAAA	TCAACGGGAC	TITCCAAAAT	GTCGTAACAA
8551	CTCCGCCCCA	TTGACGCAAA	Tegecegtag	GCGTGTACGG	TGGGAGGTCT
8601	ATATAAGCAG	AGCTCTCTGG	CTAACTAGAG	AACCCACTGC	TTACTGGCTT
8651	ATCGAAATTA	ATACGACTCA	CTATAGGGAG	ACCCAAGCTT	

## FIG. 19A Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

pD17-hG1b	60	120	180	240	300	360	420	480	540	600
	GGTCAATCGA	CCTGGCACCC	GGACTACTTC	GCACACCTIC	CGTGCCCTCC	CAACACCAAG	TGGRAGCCAG	GCAGCAAGGC	TCAGGGAGAG	CTAACCCAGG
	CCAGTTAGCT	GGACCGTGGG	CCTGATGAAG	CGIGIGGAAG	GCACGGGAGG	GITGIGGIIC	ACCTTCGGTC	CGTCGTTCCG	AGTCCCTCTC	GAITIGGGICC
Ġ.	50	110	170	230	290	350	410	470	530	590
	CTAGATAACC	CGGTCTTCCC	GCCTGGTCAA	CCAGCGGCGT	GCGTGGTCAC	ACAAGCCCAG	GGGTGTCTGC	CCAGTCCAGG	CCACTCATGC	CTAGGTGCCC
	GATCTATTGG	GCCAGAAGGG	CGGACCAGTT	GGTCGCCGCA	CGCACCAGTG	TOTTCGGGTC	CCCACAGACG	GGTCAGGTCC	GGTGAGTACG	GATCCACGGG
	40	100	160	220	280	340	400	460	520	580
	TCTCGAGTCT	AAGGGCCAT	GCCCTGGGCT	GGCGCCCTGA	TCCCTCAGCA	AACGIGAAIC	CAGGGAGGGA	CTATGCAGCC	TCTGCCCGCC	CAGGCACAGG
	AGAGCTCAGA	TTCCCGGGTA	CGGGACCCGA	CCGCGGGACT	AGGGAGTCGT	TIGCACTIAG	GTCCCTCCCT	GATACGTCGG	AGACGGGCGG	GTCCGTGTCC
	30	90	150	210	270	330	390	450	510	570
	TCTCCTTAGG	TGCTAGCACC	GGGCACAGCG	GTGGAACTCA	AGGACTCTAC	CTACATCTGC	GAGGCCAGCA	CGCATCCCGG	CCCGGAGGCC	AGGCTCTGGG
	AGAGGAATCC	ACGATCGTGG	CCCGTGTCGC	CACCTTGAGT	TCCTGAGATG	GATGTAGACG	CTCCGGTCGT	GCGTAGGGCC	GGGCTCCGG	TCCGAGACCC
	20	80	140	200	260	320	380	440	500	560
	TAAATTGATA	TGCGGCCG <b>CT</b>	GCACCTCTGG	TGACGGTGTC	TACAGTCCTC	GCACCCAGAC	AAGTTGGTGA	CCTGCCTGGA	TGCCTCTTCA	CITITICCCC
	ATTTAACTAT	ACGCCGGCGA	CGTGGAGACC	ACTGCCACAG	ATGTCAGGAG	CGTGGGTCTG	TTCAACCACT	GGACGGACCT	ACGGAGAAGT	GRARAAGGGG
	10	70	130	190	250	310	370	430	490	550
	GGTACCAATT	TIGGAAIICI	TCCTCCAAGA	CCCGAACCGG	CCGGCTGICC	AGCAGCITGG	GTGGACAAGA	GCTCAGCGCT	AGGCCCCGTC	GGTCTTCTGG
	CCATGGTTAA	AACCITAAGA	AGGAGGITCT	GGGCTTGGCC	GGCCGACAGG	TCGTCGAACC	CACCTGTTCT	CGAGTCGCGA	TCCGGGGCAG	CCAGAAGACC

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# FIG. 19B Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

pD17-hG1b 50 660 ra rccggagga	720 AGCTCGGACA TCGAGCCTGT	780 CCAARTCTTG GGTTTAGAAC	840 CGCCCTCCAG GCGGGAGGTC	900 CAGCCGGGTG GTCGGCCCAC	960 CCGTCAGTCT GGCAGTCAGA	1020 GAGGTCACAT CTCCAGTGTA	1080 TACGTGGACG ATGCACCTGC	1140 AGCACGTACC TCGTGCATGG	318 GAGTAC CTCATC
pD1 650 AAGAGCCATA TTCTCGGTAT	710 CCACTCCCTC GGTGAGGGAG	770 TCTGCAGAGC AGACGTCTCG	830 GCCCAGGCCT CGGGTCCGGA	890 GGACAGGCC CCTGTCCGGG	237 235 950 CCTGGGGGGA GGACCCCCT	1010 CCGGACCCCT GGCCTGGGGA	1070 GTTCAACTGG CAAGTTGACC	1130 GCAGTACAAC CGTCATGTTG	1190 GAATGGCAAG
640 CAGACCTGCC	700 GCCAAACTCT CGGTTTGAGA	760 CAATCTTCTC GTTAGAAGAG	820 AGGTAAGCCA TCCATTCGGT	880 CTGCATCCAG GACGTAGGTC	940 CACCIGAACT GIGGACTIGA	1000 TCATGATCTC AGTACTAGAG	1060 CTGAGGTCAA GACTCCAGTT	1120 CGCGGGAGGA GCGCCTCCT	1180 AGGACTGGCT TCCTGACCGA
630 Gracraseder		750 CAGTAACTCC GTCATTGAGG	810 CACCGTGCCC GTGGCACGGG	870 CTAGAGTAGC GATCTCATCG	930 TCTTCCTCAG AGAAGGAGTC	990 AAGGACACCC TTCCTGTGGG	1050 CACGAAGACC GTGCTTCTGG	1110 AAGACAAAGC TTCTGTTTCG	1170 GTCCTGCACC CAGGACGTGG
	680 GACCTAAGCC CTGGATTCGG	740 TCCCAGATTC AGGGTCTAAG	800 CACACATGCC GTGTGTACGG	860 GACAGGTGCC CTGTCCACGG	920 CACCTCCATC GTGGAGGTAG	980 CCCAAAACCC GGGTTTTGGG	1040 GGACGTGAGC CCTGCACTCG	1100 GCATAATGCC CGTATTACGG	1160 CGTCCTCACC GCAGGAGTGG
	GGGACGIGIG 670 CCCTGCCCCT GGGACGGGGA	730 CCTTCTCTCC GGAGAGAGAGG	790 TGACAAAACT ACTGTTTTGA	850 CTCAAGGCGG GAGTTCCGCC	910 CTGACACGTC GACTGTGCAG	970 TCCTCTTCCC AGGAGAAGGG	1030 GCGTGGTGGT CGCACCACCA	1090 GCGTGGAGGT CGCACCTCCA	1150 GTGTGGTCAG CACACCAGTC

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## FIG. 19C Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

1260	1320	1380	1440	1500	1560	1620	1680	1740	1800
AAAGCCAAAG	ACCCTCTGCC	ACCACAGGIG	GACCTGCCTG	GCAGCCGGAG	CCTCTACAGC	CTCCGTGATG	GGGTAAATGA	GATGCTTGGC	CCAGCGCTGC
TTTCGGTTTC	TGGGAGACGG	TGGIGICCAC	CTGGACGGAC	CGTCGGCCTC	GGAGATGTCG	GAGGCACTAC	CCCATTTACT	CTACGAACCG	GGTCGCGACG
1250	1310	1370	1430	1490	1550	1610	1670	1730	1790
AACCATCTCC	GGCTCGGCCC	AGCCCCGAGA	AGGTCAGCCT	AGAGCAATGG	GCTCCTTCTT	TCTTCTCATG	CCCTGTCTCC	GTCGCACGAG	AATAAAGCAC
TTGGTAGAGG	CCGAGCCGGG	TCGGGGCTCT	TCCAGTCGGA	TCTCGTTACC	CGAGGAAGAA	AGAAĞAGTAC	GGGACAGAGG	CAGCGTGCTC	TTATTTGGTG
31 1240	1300	1360	1420	1480	1540	1600	1660	1720	1780
CCATCGAGAA	GACAGAGGCC	CCTACAGGGC	ACCAAGAACC	GTGGAGTGGG	GACTCCGACG	CAGGGGAACG	AAGAGCCTCT	GCCTCTCGCG	CCAGCATGGA
GGTAGCTCTT	CTGTCTCCGG	GGATGTCCCG	TGGTTCTTGG	CACCTCACCC	CTGAGGCTGC	GTCCCCTTGC	TTCTCGGAGA	CCGAGAGCGC	GGTCGTACCT
1230331	1290	1350	1410	1470	1530	1590	1650	1710	1770
CTCCCAGCCC CC	GGGCCACATG	AACCTCTGTC	GGATGAGCTG	CGACATCGCC	TCCCGTGCTG	CAGGTGGCAG	CTACACGCAG	CCGCTCCCG	TCCCGGGCGC
GAGGGTCGGG GG	CCCGGTGTAC	TTGGAGACAG	CCTACTCGAC	GCTGTAGCGG	AGGGCACGAC	GTCCACCGTC	GATGTGCGTC	GGCGAGGGGC	AGGGCCCGCG
1220	1280	1340	1400	1460	1520	1580	1640	1700	1760
Caacaaagcc	TGGGGTGCGA	CCGCTGTACC	CCCCATCCCG	TCTATCCCAG	AGACCACGCC	TGGACAAGAG	TGCACAACCA	CGGCAAGCCC	TGTACATACT
gtygtytogg	ACCCCACGCT	GGCGACATGG	GGGGTAGGGC	AGATAGGGTC	TCTGGTGCGG	ACCTGTTCTC	ACGTGTTGGT	GCCGTTCGGG	ACATGTATGA
322 1210	1270	1330	1390	1450	1510	1570	1630	1690	1750
GCAAGGTCTC	GTGGGACCCG	CTGAGAGTGA	TACACCCTGC	GTCAAAGGCT	AACAACTACA	AAGCTCACCG	CATGAGGCTC	GTGCGACGGC	ACGTACCCCC
CGTTCCAGAG	CACCCTGGGC	GACTCTCACT	ATGTGGGACG	CAGTTTCCGA	TTGTTGATGT	TYCGAGTGGC	GTACTCCGAG	CACGCTGCCG	TGCATGGGGG

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# FIG. 19D Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

pD17-hG1b so sr creasscers ca sacreesac	1920 GCTGTGCAGG CGACACGTCC	1980 GGTGGGGGAT CCACCCCTA	2040 GGAAGCCCTA CCTTCGGGAT	2100 TGTTCTGTGA ACAAGACACT	2160 GCGGTGGGCT CGCCACCCGA	2220 CACGCGCCCT GTGCGCGGGA	2280 GCTACACTTG CGATGTGAAC	2340 ACGITCGCCG TGCAAGCGGC	2400 AGIGCITIAC TCACGARAIG
pD1 1850 caggccgagr grccggcrca	1910 ACTGGCCCAG TGACCGGGTC	1970 CCCTCGGCAG GGGAGCCGTC	2030 CTGGGCCACG GACCCGGTGC	2090 GAGACTGTCC CTCTGACAGG	2150 TGCTGGGGAT ACGACCCTA	2210 GGGGTATCCC CCCCATAGGG	2270 CAGCGTGACC GTCGCACTGG	2330 CITICICGCC GAAAGAGCGG	2390 GITCCGAITE CAAGGCTAAA
1840 TTCCACGGGT AAGGTGCCCA	1900 CTGTCCCCAC GACAGGGGTG	1960 CCAGGGGCTG GGTCCCCGAC	2020 CTGCCCTGGG GACGGGACCC	2080 GCCTCTGTAG CGGAGACATC	2140 CTCGGGGGCA GAGCCCCCGT	2200 GGGGCTCTAG CCCCGAGATC	2260 TGGTTACGCG ACCAATGCGC	2320 TCTTCCCTTC AGAAGGGAAG	2380 TCCCTTTAGG AGGGAAATCC
1830 TGATGGTTCT ACTACCAAGA	1890 GCGGGTCCCA CGCCCAGGGT	1950 TGGGGCTCAG ACCCCGAGTC	2010. CCAGCAGCAC GGTCGTCGTG	2070 CACAGCCCT GTGTCGGGGA	2130 TCCATGCCCA AGGTACGGGT	2190 AGAACCAGCT TCTTGGTCGA	2250 GCGCCACACC	2310 CCTTTCGCTT GGRARGCGRA	2370 AATCGGGGCA TTAGCCCCGT
1820 TGCGAGACTG ACGCTCTGAC	1880 GGGAGGCAGA CCCTCCGTCT	1940 CCCCTAGGG GGGGGATCCC	2000 GGCCCTCCCT CCGGGAGGGA	2060 GGGACAGACA CCCTGTCTGT	2120 CCTCCCBACC GGAGGGCTGG	2180 TGAGGCGGAA ACTCCGCCTT	2240 ATTAAGCGCG TAATTCGCGC	2300 AGCGCCGCT TCGCGGGCGA	2360 TCAAGCTCTA AGTTCGAGAT
1810 CCTGGGCCCC GGRCCCGGGG	1870 AGTGGCATGA TCACCGTACT	1930 TGTGCCTGGG ACACGGACCC	1990 TTGCCAGCGT AACGGTCGCA	2050 GGAGCCCTG CCTCGGGGAC	2110 GCGCCCCTGT CGCGGGGACA	2170 CIATGGCTTC GATACCGAAG	2230 GTAGCGGCGC CATCGCCGCG	2290 CCAGCGCCT GGTCGCGGGA	2350 GCTTTCCCCG CGAAAGGGGGC

FIG. 19E
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

CCATCGCCT	2520 GGACTCTTGT CCTGAGAACA	2580 TAAGGGATTT ATTCCCTAAA	2640 AACGCGAATT TTGCGCTTAA	2700 CAGGCAGGCA GTCCGTCCGT	2760 Ctaactccgc Gattgaggcg	2820 TGACTAATTT ACTGATTAAA	2880 AAGTAGTGAG TTCATCACTC	2940 GCTGCGATTT CGACGCTAAA	3000 CCCGCTGCCA
ACCINCIOGO TOCATCACCC	2510 CITIAAIAGI GAAAITATCA	2570 TITTGATITA AAAACTAAAT	2630 ACAAAATIT TGITITIAAA	2690 CCAGGCTCCC GGTCCGAGGG	2750 AGTCCCGCCC TCAGGGCGGG	2810 GCCCCATGGC CGGGGTACCG	2870 GCTATTCCAG CGATAAGGTC	ACAGCI	2990 GGATTITATC CCTAMAATAG
2440 STOATGOITC CACTACCAAG	2500 AGTCCACGIT TCAGGIGCAA	2560 CGGTCTATTC GCCAGATAAG	2620 AGCTGATTIA TCGACTAAAT	2680 TGGAAAGTCC ACCTTTCAGG	2740 CAGCAACCAT GTCGTTGGTA	2800 CCCATTCTCC GGGTAAGAGG	2860 CGGCCTCTGA GCCGGAGACT	2920 AAAAGCTTGG TTTTCGAACC	2980 AAGGCTGGTA TTCCGACCAT
<del></del>	2490 ITGACGITGG	2550 AACCCIAICT TIGGGAIAGA	2610 TTAAAAAATG AATITITIAC	2670 AGITAGGGIG TCAAICCCAC	2730 CTCAAITAGI GAGITAAICA	2790 CCCAGITICCG GGGICAAGGC	2850 GAGGCCGCCT CTCCGGCGGA	2910 GGCTTTTGCA CCGAAAACGT	2970 TCCTAGCGTG AGGATCGCAC
	-	2540 NACAACACTC TTGTTGTGAG	2600 GGCCIATIGG CCGGATAACC	2660 AATGTGTGTC TTACACACAG	2720 AAGCATGCAT TTCGTACGTA	2780 CCTAACTCCG GGATTGAGGC	2840 TGCAGAGGCC ACGTCTCCGG	2900 TGGAGGCCTA ACCTCCGGAT	2960 TTGACGGCAA AACTGCCGTT
2410 GGCACCTCGA CCGTGGAGCT	2470 GATAGACGGT 7 CTATCTGCCA 1	2530 TCCAAACTGG AGGTTTGACC	2590 TGGGGATTTC ACCCTAAAG	2650 AATTCTGTGG TTAAGACACC	2710 GANGTATGCA CTTCATACGT	2770 CCATCCCGCC GGTAGGGCGG	2830 TITITATITA AAAATAAAT	2890 GAGGCTTTT CTCCGAAAAA	2950 CGCGCCAAAC GCGCGGTTTG
	CCCCRAAAAA CTIGATIAGG GIGARGGITC ACGIAGIGGG GGGGITITITI GAACIAAICC CACIACCAAG IGCAICACC	CCCCAAAAA CTIGATIAGG GTGATGGITC ACGIAGIGGG CCATCG GGGGTTTTTT GAACTAAICC CACIACCAAG TGCATCACC GGTAGG TGCATCGCC GGTAGG TGCATCGC GGTAGG TGCATCGC TTTTCGCCCT TTGACGTGG AACTCCACGTT CTTTAAIAGI GGACTC TCAGGIGCAA GAAATTAICA CCTGAG	CCCCAAAAA CTTGATTAGG GTGATGGTTC ACGTAGTGGG GGGGTTTTTT GAACTAATCC CACTACCAAG TGCATCACCC 2480 2540 2550 2510 TTTTCGCCCT TTGACGTTGG AGTCCACGTT CTTTAATAGT AAAAGCGGGA AACTGCAACC TCAGGTGCAA GAAATTATCA 1 AACAACACC 1 AACCCTATCT CGGTCTATTC TTTTGATTTAATAGT 1 TTGTTGTGAG TTGGGATAGA GCCAGATAAAT 1 TTGTTGTGAG TTGGGATAGA GCCAGATAAAT	CCCCAAAAAA  CTTTCGCCCT  AACACCACC  AACCCTATCT  AACACCACC  TTGTTGTGTGTGT  AACACCACCT  TTGTTGTGTGTGT  AACACCACCT  AACACCACCT  AACCCTATCT  AACAACACCT  TTGTTGTGTGTGT  AACACCTATCT  AACAACACT  AACCCTATCT  AACAACACT  AACCCTATCT  AACAACACT  AACCCTATTT  AACAACACT  CGGTCTATTTA  AACACCTATTT  AACAAAAATT  CGGTCTATTTA  AACGCG  AACCCTATTTA  AACCCTATTTA  AACGCG  AACCCTATTTA  AACGCG  AACCCTATTTA  AACGCGATAAAATTT  AACGCG  AACCCTATTTA  AACGCG  AACCCTATTA  AACGCG  AACCCTATTTA  AACGCG  AACCCTATTA  AACCCTATTA  AACGCG  AACCCTATTA  AACGCG  AACCCTATTA  AACGCG  AACCCTATTA  AACGCG  AACCCTATTA  AACCCTATTA	CCCCAAAAA CTTGATTAGG GTGATGGTTC AGGTAGTGGG CCATCGG GGGGTTTTTT GACTAATCC CACTACCAAG TGCATCACC GGTAGC  2480 TTTTCGCCCT TTGACGTTGG AGTCCACGTT CTTTAATAGT GGACTC AAAAGCGGGA AACTGCAACT AAAAGCGGGA AACTGCAACT AACCCTATCG AACTGCTATCT AACACACTCT AACACACTACT AACACACTACTAC AACTGCTATTC AACCCTATTTT AACACATTTTAAAAATTG ACCTGATTAAAATTT AACACACTATTTAAAAATTG ACCTGATTTAAAAATTT AACTGCTATTTTAC CCGGATTAACC AATTTTTTAC CCGGATTAACC AATTTTTTAC CCGGATTACC ACCTGATGGGT ACCTGATGG AATTTTTAAAAATTG TCGACTAAAATTT TTGCGC AATTTTTAAAAATTT AACTGCGAGGT AATTTTTAAAAATTT AACTGCGAGGTCCC AATTTTTAAAAATTT AACTGCGAGGTCC AATTTTTAAAAATTT AACTGCGAGGTCCC AATTTTTAAAAATTT AACTGCGAGGTCCC AATTTTTAAAAATTT AACTGCGAGCTCCC AATTTTTAAAAATTT AACTGCGAGCTCCC AATTTTTAAAAATTT AACTGCGAGCTCCC AATTTTTAAAAATTT AACTGCGAGCTCCC AATTTTTAAAAATTT AACTGCGAGCTCCC AATTTTTAAAAAATTT AACTGCGAGCTCCC AACTGCAAAAATTT AACTGCGAGCTCCC AATTTTTAAAAAATTT AACTGCGAGCTCCC AATTTTTAAAAAATTT AACTGCGAGCTCCC AATTTTTAAAAAATTT AACTGCGAGCTCCCC AATTTTTAAAAAATTT AACTGCGAGCTCCCC AATTTTTAAAAAATTT AACTGCCAAAAAATTT AACTGCCAAAAAATTTAAAAATTT AATTCCCC AATTTTTAAAAAATTTAAAAAATTAAAAAATTAAAAAATTAAAA	CCCCAAAAA CTTGATTAGG GTGATGGTTC ACGTACTGGG CCATCGG GGGGTTTTTTT GAACTTAGG CTGATGGTTC CACTACCAAG TGCATCACCC GGTAGCGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT CTTTAATAGT GGACTCT TTTTTTTTTT	CCCCAAAAA CTICATINGG GTCATCAAG TGCATCTGGG GCATCGG GGGGTTTTTT GAACTAATCC CACTACCAAG TGCATCTCC GGTAGCG AAAAGCGGGA AACTGCAAC TCAGGTGCAAC CTICAGAACTCCC GGTAGCG TTGACGTTGG AATTTTTTAC CGGTCTATTC AAAACTGAAA TTGCCC TTGACATAATCC AATTTTTTAC TCACTAATAT TGTTCCC AATTTTTTACCCAC AATTTTTTAC TCACTAATAT TGTTCCC AATTTTTTACCCAC AATTTTTTAC TCACTAATAT TGTTCCC AATTTTTTACCACACAC AATTTTTAC TCACTAATAT TGTTTTTAAA TTGCCC AATTTTTTACCACACAC ACCTTTACACACACA TGTTTTTAAA TTGCCCACACACACACACACACACACACACACACACACAC	CCCCAAAAA CTTGATTAGG GTGANGGITC AGGTAGGGG CCATGGG GGGGTTTTTTTTTTTTTTTTTTTTTTTTTTTT	2420

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#### FIG. 19F Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

pD17-hG1b 3060 30 AITGGCAAGA CC IAACCGITCI	3120 AGAATGACCA TCTTACTGGT	3180 ACCTGGITCI IGGACCAAGA	3240 AGTAGAGAAC TCATCTTIG	3300 GCCTTAAGAC CGGAATTCTG	3360 GGAGGCAGTT CCTCCGTCAA	3420 ACAAGGATCA TGTTCCTAGT	3480 TATAAACTTC ATATTTGAAG	3540 AAGTATAAGT TTCATATTCA	3600 GCTCCCCTCC CGAGGGAGG
pD17 3050 AATATGGGG A	3110 GTACTTCCAA A	3170 GGGTAGGAAA 2	3230 TATAGITCTC ATATCAAGAG	3290 TITGGATGAT AAACCTACTA	3350 TIGGATAGIC AACCIAICAG	3410 ACTCTTIGIG TGAGAAACAC	3470 TITGGGGAAA AAACCCCTIT	3530 AAAAGGCATC TTTTCCGTAG	3590 CAAGTTCTCT GTTCAAGAGA
3040	3100	3160	3220	3280	3340	3400	3460	3520	3580
CCGTGTCCCA	ACGAGIICAA	TGGTGATTAT	ACAGAATTAA	TTGCCAAAAG	TACACATGGI	GCCACCTTAG	CAGAAATTGA	TCCAGGAGGA	AAGATGCTTT
GGCACAGGGT	TGCICAAGII	ACCACTAATA	TGTCTTAATT	AACGGTTTTC	ATCTGIACCA	CGGTGGAATC	GTCTTTAACT	AGGTCCTCCT	TTCTACGAAA
3030	3090	3150	3210	3270	3330	3390	3450	3510	3570
TGCATCGTCG	CCGCTCAGGA	AAACAGAATC	CCTTTAAAGG	GCTCATTTTC	GCAAGTAAAG	AATCAACCAG	ACGITITIC	CTCTCTGAGG	GACTAACAGG
ACGTAGCAGC	GGCGAGTCCT	TTTGTCTTAG	GGAAATTTCC	CGAGTAAAAG	CGTTCATTTC	TTAGTTGGTC	TGCAAAAAGG	GAGAGACTCC	CTGATTGTCC
3020	3080	3140	3200	3260	3320	3380	3440	3500	3560
ACCAITGAAC	ACCCTGGCCT	AGIGGAAGGI	GAAGAATCGA	ACCACGAGGA	ACCGGAATTG	GGAAGCCATG	Tgaaagtgac	CCCAGGCGTC	CGAGAAGAAA
TGGIAACTIG	TGGGACCGGA	TCACCITICCA	CTTCTTAGCT	TGGTGCTCCT	TGGCCTTAAC	CCTTCGGTAC	Actitcactg	GGGTCCGCAG	GCFCTTCTTT
3010	3070	3130	3190	3250	3310	3370	3430	3490	3550
TCATGGTTCG	ACGGAGACCT	CAACCTCTIC	CCATTCCTGA	TCAAAGAACC	TTATTGAACA	CIGITIACCA	TGCAGGAATT	TCCCAGAATA	TYGAAGTCTA
AGTACCAAGC	TGCCTCTGGA	GTIGGAGAAG	GGTAAGGACT	AGTTTCTTGG	AATAACTTGT	GACAATGGI	ACGTCCTTAA	AGGGTCTTAT	AACTYCAGAT

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## FIG. 19G Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

3660	3720	3780	3840	3900	3960	4020	4080	4140	4200
TCTTTGTGAA	TITAAAGCIC	TAATTGITIG	ATGCCITIAA	CTACTGCTGA	AGGACTITCC	THECHIGGIT	TGGAAAATA	TITITICITAC	GTACCTTTAG
AGAACACTT	AAAITICGAG	ATTAACAAAC	TACGGAAATT	GATGACGACT	TCCTGAAAGG	AACGAACGAA	ACCTTTTTAT	AAAAAGAATG	CATGGAAATC
3650	3710	3770	3830	3890	3950	4010	4070	4130	4190
GCTTTAGATC	CCTACAGAGA	CTACTGATIC	CAGTGGTGGA	GATGATGAGG	GAAGACCCCA	AATAGAACIC	AAGAARATTA	AACATACTGT	CRAMARTIGI
CGAAATCTAG	GGATGICICI	GATGACTAAG	GTCACCACCT	CTACTACTCC	CTTCTGGGGT	TTATCETIGAG	TTCTTTTRAT	TTGTATGACA	GITTITAACA
3640	3700	3760	3820	3880	3940	4000	4060	4120	4180
ACITITGCIG	GGACAACTA	ATGTGTFAAA	TGAATGGGAG	GCCATCTAGT	GAGAAAGGIA	TGTGTTTAGT	ACTGCTATAC	TIATAATCAT	TAACTATGCT
TGAAAACGAC	CCTGTTTGAT	TACACAATTT	ACTTACCCTC	CGGTAGATCA	CTCTTICCAI	ACACAAATCA	TGACGATATG	AATATTAGTA	ATTGATACGA
3630	3690	3750	3910	3870	3930	3990	4050	4110	4170
AGACCATGGG	TCACATATT	TAAGIGIAIA	ATGGAACTGA	CAGAAGAAAT	Caaaaaagaa	TGAGICATGC	AAAAAGCIGC	GGCATAACAG	CIGCIAITAA
TCTGGTACCC	ACTOTATTAA	ATICACAIAI	TACCTTGACT	GTCTTTTA	Giitteicit	ACTCAGTACG	TITITCGACG	CCGTATTGTC	GACGATAAIT
3620	3680	3740	3800	3860	3920	3980	4040	4100	4160
CATTITIATA	TTCTGTGGTG	Ataratitit	ATTCCAACCT	CTGTTTTGCT	TCTACTCCTC	CTAAGTIFFT	ACCACAAAGG	TITATAAGTA	CATACAGTGT
GIAAAAATAT	AAGACACCAC	Tatittaar	TAAGGTTGGA	GACAAAACGA	AGATGAGGAG	GATTCAAAAA	TOGTOTTTCC	AAATATICAT	GTATCTCACA
3610	3670	3730	3790	3850	3910	3970	4030	4090	4150
TAAAGCIAIG	GGAACCTIAC	TAAGGIAAAT	TGTATTTAG	TGAGGAAAAC	CTCTCAACAT	TTCAGAATTG	TGCIATITAC	TTCTGTAACC	TCCACACAGGG
ATTICGAIAC	CCTTGGAATG	ATTCCAITTA	ACATAMANTC	ACTCCTTTTG	GAGAGTIGTA	AAGTCTTAAC	ACGNIAAATG	AAGACATTGG	AGGTGTCCC

# FIG. 19H Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

pD17-hG10	4260 TGACTAGAGA ACTGATCTCT	4320 CTCCCACACC GAGGGTGTGG	4380 TTTATTGCAG AAATAACGTC	4440 GCATTTTTT CGFRARARA	4500 GTCTGGATCG CAGACCTAGC	4560 CCCAACTIGT GGGTTGAACA	4620 ACAATAAAG TGFFTAFFTC	4680 TCTTATCATG AGAATAGTAC	4740 CTGTTTCCTG GACAAAGGAC	4800 ATAAAGTGTA TATTTCACAT
<u>.</u>	4250 TATAGTGCCT	4310 TTTAAAAAAC AAATTTTTG	4370 TOTTAACTIG ACAATTGAAC	4430 CACAAATAAA GTGTTTATTT	4490 ATCTTATCAT TAGAATAGTA	4550 CTTCGCCCAC GAAGCGGGTG	4610 CACAAATTTC GTGTTTAAAG	4670 CATCAATGTA GTAGTTACAT	4730 ATGGTCATAG TACCAGTATC	4790 AGCCGGAAGC TCGGCCTTCG
	4240 ATATTTGATG 7 TATAAACTAC 2	4300 TTTACTTGC	4360 CAATTGTTGT GTTAACAACA	4420 TCACAAATTT AGTGTTTAAA	4480 TCATCAATGT AGTAGTTACA	4540 TGCTGGAGTT ACGACCTCAA	4600 GCAATAGCAT CGTTATCGTA	4660 TGTCCAAACT ACAGGTTTGA	4720 TGGCGTAATC ACCGCATTAG	4780 ACAACATACG TGTTGTATGC
	4230 TTRATARGGA AATTATTCCT	4290 TTTGTAGAGG	4350 AAAATGAATG TTTTACTTAC	4410 AGCAATAGCA TCGTTATCGT	4470 TTGTCCAAAC AACAGGTTTG	4530 GGGGATCTCA CCCCTAGAGT	4590 TACAAATAAA ATGTTTATTT	4650 AGTTGTGGTT TCAACACCAA	4710 AGCTAGAGCT TCGATCTCGA	4770 ACAATTCCAC TGTTAAGGTG
	4220 TGTAAAGGGG 3 ACATTTCCCC 3	4280 CCATACCACA GGTATGGTGT	4340 CCTGAAACAT GGACTTTGTA	4400 TTACAAATAA AATGTTTATT	4460 TAGTTGTGGT ATCAACACCA	4520 CCTCCAGCGC GGAGGTCGCG	4580 TTATAATGGT AATATTACCA	4640 ACTGCATTCT TGACGTAAGA	4700 GTCGACCTCT CAGCTGGAGA	4760 TTATCCGCTC AATAGGCGAG
	4210 CTTTTTAATT 7 GAAAAATTAA	4270 TCATAATCAG (	4330 TCCCCTGAA AGGGGGACTT	4390 CTTATAATGG GAATATTACC	4450 CACTGCATTC GTGACGTAAG	4510 GCTGGATGAT CGACCTACTA	4570 TTATTGCAGC AATAACGTCG	4630 CATTITITC GTAAAAAAG	4690 TCTGTATACC AGACATATGG	4750 TGTGAAATTG ACACTTTAAC

FIG. 19I Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

;	pD17-hG1b 50 4860 gc rcacrgccco cg agraacgggc	4920 CGCGCGGGGA GCGCGCCT	4980 CTGCGCTCGG GACGCGAGCC	5040 TTATCCACAG AATAGGTGTC	5100 GCCAGGAACC CGGTCCTTGG	5160 GAGCATCACA CTCGTAGTGT	5220 TACCAGGCGT ATGGTCCGCA	5280 ACCGGATACC TGGCCTATGG	5340 TGTAGGTATC ACATCCATAG	5400 CCCGTTCAGC GGGCAAGTCG
	pD1 4850 recerrecec	4910 AATCGGCCAA TTAGCCGGTT	4970 CACTGACTCG GTGACTGAGG	5030 GGTAATACGG CCATTATGCC	5090 CCAGCAAAAG GGTCGTTTTC	5150 CCCCCTGAC GGGGGAACTG	5210 ACTATARAGA TGATATITCT	5270 CCTGCCGCTT GGACGGCGAA	5330 ATGCTCACGC TACGAGTGCG	5390 GCACGAACCC CGTGCTTGGG
	4840 TCACATTAAT 7 AGTGTAATTA 1	4900 IGCATTAATG ACGTAATTAC	4960 CTTCCTCGCT GAAGGAGCGA	5020 ACTCAAAGGC TGAGTTTCCG	5080 GAGCAAAAGG CTCGTTTTCC	5140 ATAGGCTCCG TATCCGAGGC	5200 ACCCGACAGG TGGGCTGTCC	5260 CTGTTCCGAC GACAAGGCTG	5320 CGCTTTCTCA GCGAAAGAGT	5380 TGGGCTGTGT ACCCGACACA
	4830 GTGAGCTAAC CACTCGATTG	4890 TCGTGCCAGC 7	4950 CGCTCTTCCG GCGAGAAGGC	5010 GTATCAGCTC CATAGTCGAG	5070 AAGAACATGT TTCTTGTACA	5130 GCGTTTTTCC CGCARARAGG	5190 AGGTGGCGAA TCCACCGCTT	5250 GTGCGCTCTC CACGCGAGAG	5310 GRANGCGTGG CCTTCGCACC	5370 CGCTCCAAGC GCGAGGTTCG
	4820 TGCCTAATGA G ACGGATTACT C	4880 GGGAAACCTG 7 CCCTTTGGAC 1	4940 GCGTATTGGG CGCATAACCC	5000 GCGGCGAGCG CGCCGCTCGC	5060 TAACGCAGGA ATTGCGTCCT	5120 CGCGTTGCTG GCGCAACGAC	5180 CTCAAGTCAG GAGTTCAGTC	5240 AAGCTCCCTC TTCGAGGGAG	5300 TCTCCCTTCG AGAGGGAAAGC	5360 GTAGGICGII CAICCAGCAA
	4810 PAGCCTGGGG T	4870 CTTTCCAGIC GARAGGICAG	4930 GAGGCGGTTT CTCCGCCAAA	4990 TCGTTCGGCT AGCAAGCCGA	5050 AATCAGGGGA TFAGTCCCCT	5110 GTAAAAGGC CATTITTCCG	5170 ANANICGACG TITTAGCIGC	5230 TICCCCCTGG	5290 TGTCCGCCTT ACAGGCGGAA	5350 TCAGTTCGGT AGTCAAGCCA

FIG. 19J
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

01:5-1-7-LO	5460	5520	5580	5640	5700	5760	5820	5880	5940	6000
	AGACACGACT	GIAGGCGGIG	GTATTTGGTA	TGATCCGGCA	ACGCGCAGAA	CAGTGGAACG	ACCTAGATCC	ACTIGGICIG	TIFICGIICAT	TTACCATCTG
	TCTGTGCTGA	CATCCGCCAC	CATAAACCAT	ACTAGGCCGT	TGCGCGTCTT	GTCACCTTGC	TGGATCTAGG	TGAACCAGAC	AAAGCAAGIA	AATGGTAGAC
፭	5450	5510	5570	5630	5690	5750	S810	5870	5930	5990
	CAACCCGGTA	AGCGAGGTAT	TAGAAGGACA	TGGTAGCTCT	GCAGCAGAIT	GICTGACGCI	AAGGATCTTC	ATATGAGTAA	GATCTGTCTA	ACGGGAGGGC
	GTTGGGCCAT	TCGCTCCATA	ATCITCCTGI	ACCATCGAGA	CGTCGTCIAA	CAGACTGCGA	TTCCTAGAAG	TATACTCATT	CTAGACAGAT	TGCCCTCCCG
	5440	5500	5560	5620	5680	5740	5900	5860	5920	5980
	GTCTTGAGIC	GGATTAGCAG	ACGGCTACAC	Gararagagt	TTGTTTGCAA	TTTCTACGGG	GATTATCAAA	TCTAAAGTAT	CTATCTCAGC	TAACTACGAT
	CAGAACTCAG	CCTAATCGTC	TGCCGATGTG	Ctttttctca	AACAAACGTT	AAAGATGCCC	CTAATAGTTT	AGATTTCATA	GATAGAGTCG	ATTGATGCTA
	5430	5490	5550	5610	S670	5730	5790	5850	5910	5970
	GOTAACTATC	ACTGGTAACA	TGGCCTAACT	GTTACCTTCG	GGTGGTTTTT	CCTTTGATCT	TTGGTCATGA	TITAAAICAA	AGTGAGGCAC	GTCGTGTAGA
	CCATTGATAG	TGACCATTGT	ACCGGATTGA	CAATGGAAGC	CCACCAAAAA	GGAAACTAGA	AACCAGTACT	AAAIITAGII	TCACTCCGTG	CAGCACATCT
	5420	5480	5540	5600	5660	5720	5780	5840	5900	5960
	CGCCTTATCC	GGCAGCAGCC	CTTGAAGTGG	GCTGAAGCCA	CGCTGGTAGC	TCAAGAAGAT	TTAAGGGATT	AAAATGAAGT	ATGCTTAATC	CTGACTCCCC
	GCGGAATAGG	CCGTCGTCGG	GAACTTCACC	CGACTTCGGT	GCGACCATCG	AGTTCTTCTA	AATTCCCTAA	TTTTACTTCA	TACGAATTAG	GACTGAGGGG
	5410 CCGACCGCTG GGCTGGCGAC	5470 TATCGCCACT ATAGCGGTGA	5530 CTACAGAGIT GATGICICAA	5590 TCTGCGCTCT AGACGCGAGA	5650 AACAAACCAC TTGTTTGGTG	5710 AAAAAGATC TTTTTCCTAG	5770 AAAACICACG TITIGAGIGG	5830 TITAAATTITAAATTA	5890 ACAGITACCA TGICAATGGI	5950 CCATAGTIGC GGTATCAACG

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# FIG. 19K Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

pD17-hG1b 50 6060	TTATCAGCAA AATAGTCGTT	6120 TCCGCCTCCA AGGCGCAGGT	6180 AATAGTTTGC TTATCAAACG	6240 GGTATGGCTT CCATACCGAA	6300 Tigiccaaaâ Aacaccitti	6360 GCAGIGITAT CGICACAAIA	6420 GTAAGATGCT CATTCTACGA	6480 CGGCGACCGA GCCGCTGGCT	6540 ACTITARANG TORANITITC	6600 CCGCTGITGA GCCGACAACT
pD1	GGCTCCAGAT	6110 TGCAACTTTA ACGTTGAAAT	6170 TTCGCCAGTT AAGCGGTCAA	6230 CICGICGITI GAGCAGCAAA	6290 ATCCCCCATG TAGGGGGTAC	6350 TAAGTTGGCC ATTCAACCGG	6410 CATGCCATCC GTACGGTAGG	6470 ATACIQIATG TATCACATAC	6530 ACATAGCAGA TGTATCGTCT	6590 AAGGATCITA TICCIAGAAT
6040	-	6100 GAAGTGGTCC CTTCACCAGG	6160 GAGTAAGTAG CTCATTCATC	6220 TGGTGTCACG ACCACAGTGC	6280 GAGITACATG CTCAATGIAC	6340 TTGTCAGAAG AACAGTCTTC	6400 CICTIACTGI GAGAAIGACA	6460 CATTCTGAGA GTAAGACTCT	6520 ATACCGCGCC TATGGCGCGG	6580 Gararctee Cettegagag
O E CO		6090 GCCGAGCGCA CGGCTCGCGT	6150 CGGGAAGCIA GCCCTTCGAT	6210 ACAGGCATCG TGTCCGTAGC	6270 CGATCAAGGC GCTAGTTCCG	6330 CCTCCGATCG GGAGGCTAGC	6390 CIGCATAAIT GACGIAITAA	6450 TCAACCAGT AGTTGGTTCA	6510 ATACGGGALA TATGCCCTAT	6570 TCTTCGGGGC
0	6020 TGCAATGATA ( ACGTTACTAT	6080 AGCCGGAAGG TCGGCCTTCC	6140 TAATTGTTGC ATTAACAACG	6200 TGCCATTGCT ACGGTAACGA	6260 CGGTTCCCAA GCCAAGGGTT	6320 CTCCFTCGGT GRGGRAGCCA	6380 TATGGCAGCA ATACCGTCGT	6440 TGGTGAGTAC ACCACTCATG	6500 CCCGGCGTCA GGGCCGCAGT	6560 TGGAAAACGT ACCTTTTGCA
;	6010 GCCCCAGTGC 1 CGGGGTCACG 1	6070 TRAACCAGCC	6130 TCCAGICTAI AGGICAGAIA	6190 GCAACGIIGI CGIIGCAACA	6250 CATTCAGCTC GTAAGTCGAG	6310 AAGCGGTTAG TTCGCCAATC	6370 CACTCATGGT GTGAGTACCA	6430 TTTCTGTGAC	6490 GITGCICITG CAACGAGAAC	6550 TGCTCATCAT ACGAGTAGTA

FIG. 19L
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

	6660 TTIACITICA AAATGAAAGI	6720 GGRATAAGGG CCFTATTCCC	6780 AGCATTTATC TCGTAAATAG	6840 AAACAAATAG TITGTITATC	6900 GGAGATCTGC CCTCTAGACG	6960 TTARTITIAT AATTAAAATA	7020 GGTCGACTCT CCAGCTGAGA	7080 CITOIGIGII GAACACACAA	7140 GCTTGACCGA CGAACTGGCT	7200 NTGTACGGGC TACATGCCCG
<u>.</u>	6650 TTCAGCATCT	6710 CGCAAAAAG GCGTTTTTC	6770 ATATTATTOR TATAATAACT	6830 TTAGAAAAT AATCITITIA	6890 CGACGGATCG GCTGCCTAGC	6950 ACCITITIT TGGAAAAAA	7010 GATCCCCTAT CTAGGGGATA	7070 CTGCTCCCTG QACGAGGGAC	7130 ACAAGGCAAG TGTTCCGTTC	7190 CIGCTTCGCG GACGAAGCGC
	6640 CCAACTGATC 1 GOTTGACTAG A	6700 GGCAAATGC C	6760 TCCTTTTTCA AGGAAAAGT	6820 TTGAATGTAT AACTTACATA	6880 CACCTGACGT GTGGACTGCA	6940 AGCCAGAGIA TCGGICTCAI	7000 CCGATCTCCC GGCTAGAGGG	7060 AAGCCAGTAT TTCGGTCATA	7120 TTAAGCTACA AATTCGATGT	7180 GCGITITIGCG CGCAAAACGC
	6630 ACTCGTGCAC C TGAGCACGTG G	6690 AAAACAGGAA TTTTGTCCTT C	6750 CTCATACTCT GAGTATGAGA	6810 GGATACATAT CCTATGTATA	6870 CGAAAAGIGC GCTTTICACG	6930 GGCTTCGART CCGAAGCTTA	6990 QAGIITGGCG CICAAACCGC	7050 CCGCATAGIT GGCGTAICAA	7110 CGAGCAAAAT GCTCGTTTTA	7170 TTAGGGTTAG AATCCCAATC
	6620 GATGTAACCC A	6680 TGGGTGAGCA P	6740 ATGITGAATA TACAACITAT	6800 TCTCATGAGC AGAGTACTCG	6860 CACATTICCC GTGTAAAGGG	6920 GAGGCGCGCC CTCCGCGCGG	6980 TTTTGAGATG AAAACTCTAG	7040 TGCTCTGATG ACGAGACTAC	7100 GAGTAGTGCG CTCATCACGC	7160 AAGAATCTGC TTCTTAGACG
	6610 GATCCAGTTC Q	6670 CCAGCGITTC 7 GGTCGCAAAG 7	6730 CGACACGGAA GCTGTGCCTT	6790 AGGGTTATTG TCCCAATAAC	6850 GGGTTCCGCG	6910 TAGGTGACCT ATCCACTGGA	6970 TITATITAT AAATAAATA	7030 CAGTACAATC GTCATGTTAG	7090 GGAGGTCGCT CCTCCAGCGA	7150 Caattgcatg Gitaacgiac

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#### FIG. 19M Primary Sequence = SEQ ID NO:23 Complementary Sequence = SEQ ID NO:29

pD17-hG1b 50 7260 AA TTACGGGGTC	7320 7320 ATGGCCCGCC	7380 TTCCCATAGT AAGGGTATCA	7440 AAACTGCCCA TTTGACGGGT	7500 TCAATGACGG AGTTACTGCC	7560 CTACTTGGCA GATGAACCGT	7620 Agtacatcaa Tcatgtagtt	7680 TTGACGTCAA AACTGCAGTT	7740 ACAACTCCGC TGTTGAGGCG	7800 GCAGAGCICT CGTCTCGAGA
pD17 7250 TAGTAATCAA T		7370 ATGACGTATG TACTGCATAC	7430 TATTTACGGI ATANATGCCA	7490 CCTATTGACG GGATANCTGC	7550 TGGGACTITC ACCCTGAAAG	7610 CGGTTTTGGC GCCRRAACCG	7670 CTCCACCCCA GAGGTGGGGT	7730 AAATGICGIA TITACAGCAI	7790 GICIATATAA CAGATATAT
	AICHAIMAI 7300 CGITACATAA GCAATGTATT	7360 GACGICAAIA CTGCAGITAI	7420 ATGGGTGGAC TACCCACCTG	7480 AAGTACGCCC TTCATGCGGG	7540 CATGACCTTA GTACTGGAAT	7600 CATGGTGATG GTACCACTAC	7660 ATTTCCAAGT TAAAGGTTCA	7720 GGACTTTCCA CCTGAAAGGT	7780 ACGGTGGGAG
7230 GATTATTGAC	CIMATAACIU 7290 TGGMGTTCCG ACCTCAAGGC	7350 CCCGCCCATT GGGCGGCTAA	7410 ATTGACGTCA TAACTGCAGT	7470 ATCATATGCC TAGTATACGG	7530 ATGCCCAGTA TACGGGTCAT	7590 TCGCTATTAC AGCCATAATG	7650 ACTCACGGGG TGAGTGCCCC	7710 AAAATCAACG TTTTAGITGC	7770 GTAGGCGTGT CATCCGCACA
_	GCAACTGTAA 7280 AGCCCATATA TCGGGTATAT	7340 CCCAACGACC GGGTTGCTGG	7400 GGGACTITICC CCCTGAAAGG	7460 CATCAAGTGT GTAGTTCACA	7520 GCCTGGCATT CGGACCGTAA	7580 GIATTAGICA CATAAICAGI	7640 TAGCGGTTTG ATCGCCAAAC	7700 TTTTGGCACC AAAACCGTGG	7760 CAAATGGGCG GTTTACCCGC
_	GICTATATGC (7270 ATTAGTECAT TAATCAAGTA	7330 TGGCTGACCG ACCGACTGGC	7390 AACGCCAATA TTGCGGTTAT	7450 CTTGGCAGTA GAACCGTCAT	7510 TARATGGCCC ATTTACCGGG	7570 GTACATCTAC CATGTAGATG	7630 TGGGCGTGGA ACCGGCACCT	7690 TGGGAGTTTG ACCCTCAAAC	7750 CCCATTGACG GGGTAACTGC

FIG. 19N
Primary Sequence = SEQ ID NO:23
Complementary Sequence = SEQ ID NO:29

pD17-hG1b

CTGGCTAACT AGAGAACCCA CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG GACCGATTGA TCTCTTGGGT GACGAATGAC CGAATAGCTT TAATTATGCT GAGTGATATC

7870 GGAGACCCAA GCTT CCTCTGGGTT CGAA

7880

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FIG. 20
COMPLEMENT DEPENDENT CYTOTOXICITY

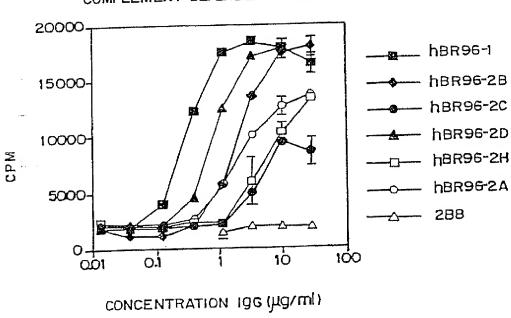
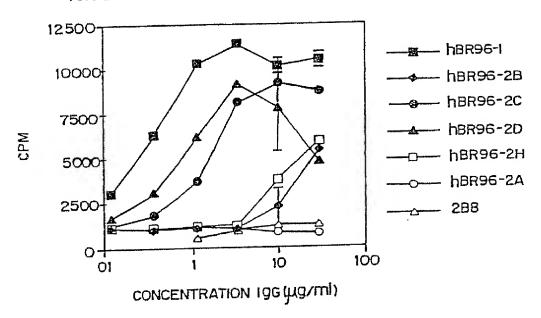


FIG. 21

### ANTIBODY DEPENDENT CELL-MEDIATED CYTOTOXICITY



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FIG.22



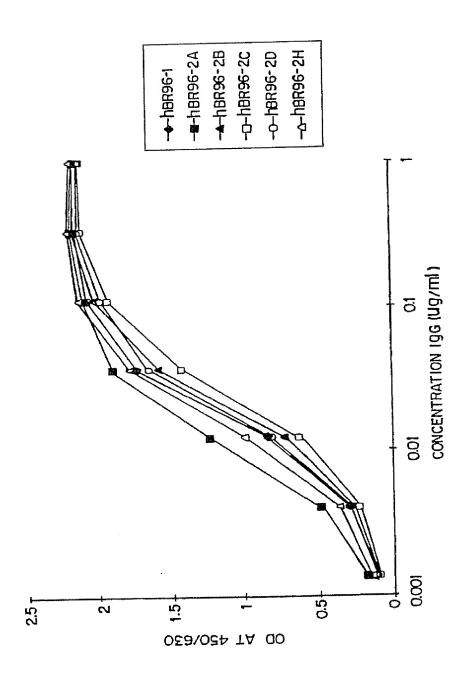


FIG.23

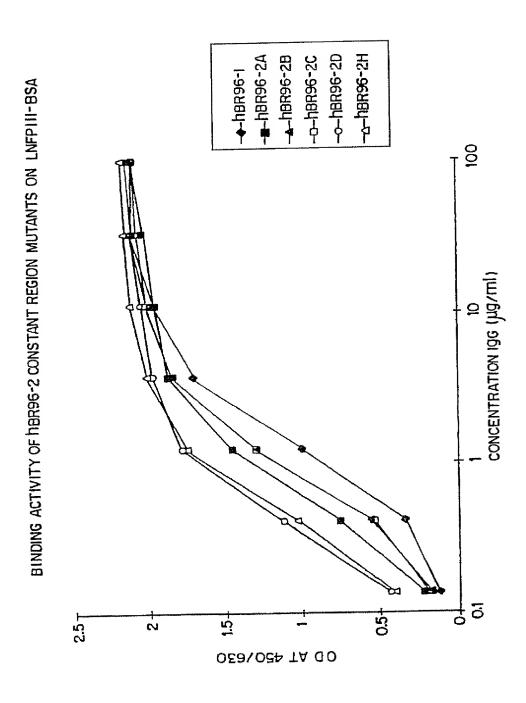


FIG. 24A

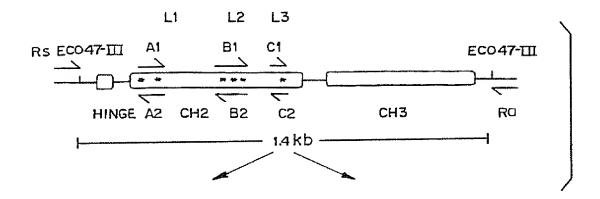
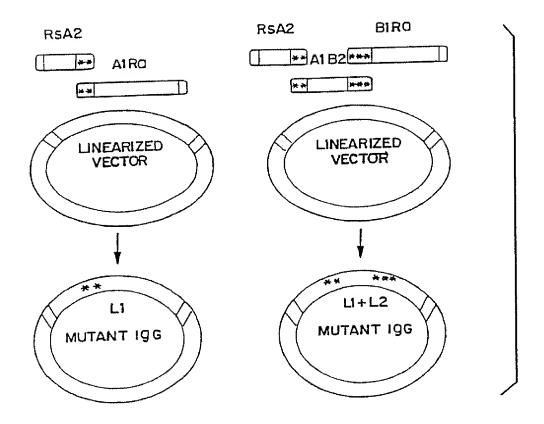
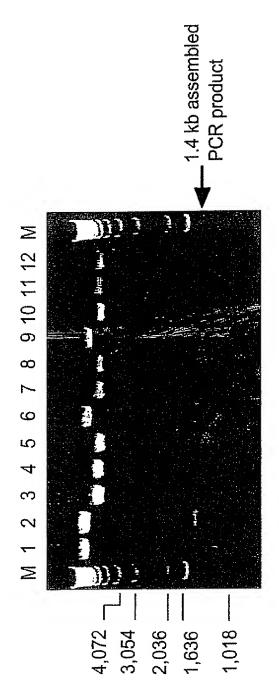


FIG. 24B



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#### FIG. 26

#### hBR96-2 Heavy Chain Variable Region (VH)

(SEQ ID NO:24)

1 11 21 31 41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVSY
51 61 71 81 91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL
101 111
ADGAWFAYWG QGTLVTVSS

Human IqGl Constant

(SEQ ID NO:25)

CH1

A STKGPSVFPL APSSKSTSGG TAALGCLVKD

YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY
CH2 235 237

ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CHAPELLGGP SVFLFPPKPK

DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS
318 320 322 331 CH3

TYRVVSVLTV LHQDWLNGKÈ YKDKVSNKAL PAPIEKTISK AKGQPREPQV

YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL

DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK

### FIG. 27

hBR96-2A: Heavy Chain Variable Region (V<sub>H</sub>)

(SEQ ID NO:24)

1 11 21 31 41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVSY
51 61 71 81 91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL
101 111
ADGAWFAYWG QGTLVTVSS

#### hBR96-2A: Human Heavy Chain IgGl Constant Region △CH2

(SEQ ID NO:26)

A STRGPSVFPL APSSKSTSGG TAALGCLVKD YFPEPVTVSW NSGALTSGVH
TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK
SCDKTHTCPP CP GQPREPQV YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA
VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM
HEALHNHYTQ KSLSLSPGK

### FIG. 28

#### (SEQ ID NO:27)

This sequence is the chi BR96 IgGl with CH2 deleted.

#### VH

- 1 EVNLVESGGG LVQPGGSLKV SCVTSGFTFS DYYMYWVRQT PEKRLEWVAY
- 51 ISQGGDITDY PDTVKGRFTI SRDNAKNTLY LQMSRLKSED TAMYYCARGL CH1
- 101 DDGAWFAYWG QGTLVTV5VA STKGPSVFPL APSSKSTSGG TAALGCLVKD
- 151 YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY
  CH3
- 201 ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPGQPREPQV YTLPPSRDEL
- 251 TKNOVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS
- 301 KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK